

From: Chan, Christina
Sent: Thursday, January 24, 2002 2:49 PM
To: Kemmerer, Elizabeth; STIC-Biotech/ChemLib
Subject: RE: rush seq search req

Please rush. Thanks Chris

-----Original Message-----

From: Kemmerer, Elizabeth
Sent: Thursday, January 24, 2002 2:27 PM
To: Chan, Christina
Subject: rush seq search req

Hi Christina-
Please approve the following for a due amended:

STIC:
Please do a regular and interferences search of SEQ ID NO: 26 (full length) and an oligo search of 30 contiguous amino acids of SEQ ID NO: 26 for 08/741095.

Thanks,

Elizabeth (Betsy) Kemmerer
Art Unit 1646
308-2673
CM1-10B17
Mailbox: 10C01

RECEIVED
JAN 24 2002
STIC

TYPE OF SEARCH:		VENDOR/COST(where applic.)
Searcher: _____	NA Sequences: _____	STN: _____
Phone: _____	AA Sequences: _____	DIALOG: _____
Location: _____	Structures: _____	Questel/Orbit: _____
Date Picked Up: <u>1/24/02</u>	Bibliographic: _____	DRLink: _____
Date Completed: <u>1/25/02</u>	Litigation: _____	Lexis/Nexis: _____
Searcher Prep/Review: _____	Full text: _____	Sequence Sys.: <u>PS</u>
Clerical: _____	Patent Family: _____	WWW/Internet: _____
Online time: _____	Other: _____	Other (specify): _____

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 24, 2002, 16:23:35 ; Search time 23.2 Seconds

(without alignments)
903.566 Million cell updates/sec

Title: US-08-741-095B-26

Perfect score: 283
Sequence: 1 MEPPGDMGPPWRSTPRTDV.....VTVVAEETIPSTGRSPNH.283

Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 522463 seqs, 74073290 residues

Word size : 0

Total number of hits satisfying chosen parameters: 237521

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Listing first 45 summaries

Database : A.GeneSeq_1101.*

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19: /SID88/gcgdata/geneSeq/geneSeq/AA1998.DAT.*
20: /SID88/gcgdata/geneSeq/geneSeq/AA1999.DAT.*
21: /SID88/gcgdata/geneSeq/geneSeq/AA2000.DAT.*
22: /SID88/gcgdata/geneSeq/geneSeq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	10	3.5	10	AAV79208	SHVEM1-Fc fusion N
2	6	2.1	8	AAJ01151	Hepatitis C virus
3	6	2.1	8	AAJ01702	Hepatitis C virus
4	6	2.1	9	AAV47926	Immunogenic peptid
5	6	2.1	9	AAJ98703	Cytotoxic T lympho
6	6	2.1	9	AAJ00162	Hepatitis C virus
7	6	2.1	9	AAJ00288	Hepatitis C virus
8	6	2.1	9	AAJ01152	Hepatitis C virus
9	6	2.1	9	AAJ01463	Hepatitis C virus
10	6	2.1	9	AAJ01758	Hepatitis C virus
11	6	2.1	9	AAJ01819	Hepatitis C virus

12	6	2.1	9	AAJ02614	Hepatitis C virus
13	6	2.1	9	AAJ03766	Hepatitis C virus
14	6	2.1	9	AAJ03901	Hepatitis C virus
15	6	2.1	10	AAJ49753	Compact structure
16	6	2.1	10	AAJ46038	Immunogenic peptid
17	6	2.1	10	AAV46444	Immunogenic peptid
18	6	2.1	10	AAJ46516	Human NF-kappa p50
19	6	2.1	10	AAJ15407	NF-kappa p50 nucle
20	6	2.1	10	AAJ88069	NF-kappa B p50 nuc
21	6	2.1	10	AAJ58923	NF-kappa B p50 nuc
22	6	2.1	10	AAJ43814	NF-kappa B p50 nuc
23	6	2.1	10	AAJ95144	Human complementar
24	6	2.1	10	AAJ03164	NF-kappa B nuclear
25	6	2.1	10	AAJ82309	NF-kappa p50 nucle
26	6	2.1	10	AAJ01007	Hepatitis C virus
27	6	2.1	10	AAJ01537	Hepatitis C virus
28	6	2.1	10	AAJ02965	Hepatitis C virus
29	6	2.1	10	AAJ03940	Hepatitis C virus
30	6	2.1	10	AAJ45928	Transdominant effe
31	6	2.1	10	AAJ35060	NF-kappa p50 nucle
32	6	2.1	11	AAJ01008	Hepatitis C virus
33	6	2.1	11	AAJ01955	Hepatitis C virus
34	6	2.1	11	AAJ02966	Hepatitis C virus
35	6	2.1	13	AAJ44066	Pulmonary surfacta
36	6	2.1	14	AAJ90379	Sequence of antiq
37	6	2.1	14	AAJ85437	Helper T-cell clas
38	6	2.1	14	AAJ82167	Human mlgE Cepilo
39	6	2.1	15	AAJ73097	Hepatitis C virus
40	6	2.1	15	AAJ00332	Hepatitis C virus
41	6	2.1	15	AAJ03277	Hepatitis C virus
42	6	2.1	15	AAJ04035	Hepatitis C virus
43	6	2.1	15	AAJ04076	Hepatitis C virus
44	6	2.1	15	AAJ04115	Hepatitis C virus
45	6	2.1	17	AAJ05596	Membrane bound Ige

ALIGNMENTS

RESULT 1	
AAV79208	standard; Peptide: 10 AA.
ID	AAV79208
AC	AAV79208;
DT	19-JUN-2000 (first entry)
DE	SHVEM1-Fc fusion N-terminal peptide.
KM	SHVEM-1: soluble herpesvirus entry mediator-1; TANGO-69-receptor;
KW	tumour necrosis factor receptor; human; herpes simplex virus;
KW	infection; cancer; inflammation; autoimmune disorder; therapy;
KW	diagnosis.
OS	Homo sapiens.
PN	WO200014230-A1.
PD	16-MAR-2000.
PF	03-SEP-1999; 99WO-US20180.
PR	03-SEP-1998; 98US-0146950.
PR	29-JUN-1999; 99US-0342767.
PA	(MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
PI	Busfield SJ;
DR	WPI: 2000-256981/22.
PT	New nucleic acid molecule encoding herpes virus entry mediator (HVEM), either in the soluble or membrane bound form, is useful in screening

PT assays and detection assays -
XX
PS Example 5; Page 127; 149pp; English.
XX

CC This sequence comprises the first 10 amino acid residues of the
CC N-terminus of a mature human TANGO-69-receptor: IgG1 Fc fusion
CC protein. The fusion protein was expressed in HEK 293T cells that
CC had been transfected with a vector carrying a gene fusion composed
CC of the human TANGO-69-receptor (SHVEN1, see AA294195) coding sequence
CC and DNA encoding the Fc domain of human IgG1. SHVEN1 (see also
CC AA179204) is a novel soluble form of membrane-bound herpesvirus entry
CC mediator (mhVEM). DNA encoding HVEMs, HVEM proteins and HVEM
CC antibodies can also be used in screening and detection assays. HVEM
CC proteins can also be used for regulation of cell proliferation,
CC cell differentiation, cell survival, inflammation mast cell
CC activity, herpes simplex virus infection and/or proliferation,
CC and/or coagulation.
XX
SQ Sequence 10 AA;

Query Match 3.5%; Score 10; DB 21; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 37 PALPSCKEDE 46
|||||
DB 1 palpsckede 10

RESULT 2
AAJ01151
ID AAJ01151 standard; Peptide; 8 AA.
XX

AC AAJ01151;

XX 02-JUL-2001 (first entry)

DE Hepatitis C virus epitope #1142.

XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
KW antiviral.

XX Hepatitis C virus.

XX WO200121189-A1.

XX PD 29-MAR-2001.

XX PF 19-JUL-2000; 2000WO-US19774.

XX PR 19-JUL-1999; 99US-0357737.

XX PA (EPLM-) EPIMMUNE INC.

XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX PI Baker DM, Celis E, Kubo RT, Grey HM;

XX DR WPI; 2001-308046/32.

XX A new composition useful as a vaccine against hepatitis C virus -

XX PS Disclosure; Page 129; 214pp; English.
XX

CC The present invention describes a composition comprising a prepared
CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
CC These are derived from HCV HLA-binding motifs. They are useful in
CC vaccines for the prevention and treatment of HCV infection in humans. The
CC present sequence is an epitope used in the disclosure of the invention.
XX
SQ Sequence 8 AA;

Query Match 2.1%; Score 6; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 145 SPQGRV 150
|||||
DB 1 spqgrv 6

RESULT 3

AAJ01702
ID AAJ01702 standard; Peptide; 8 AA.

XX AC AAJ01702;

XX DT 02-JUL-2001 (first entry)

XX DE Hepatitis C virus epitope #1693.

XX KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
KW antiviral.

XX OS Hepatitis C virus.

XX PN WO200121189-A1.

XX PD 29-MAR-2001.

XX PF 19-JUL-2000; 2000WO-US19774.

XX PR 19-JUL-1999; 99US-0357737.

XX PA (EPLM-) EPIMMUNE INC.

XX PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
XX PI Baker DM, Celis E, Kubo RT, Grey HM;

XX DR WPI; 2001-308046/32.

XX A new composition useful as a vaccine against hepatitis C virus -

XX PS Disclosure; Page 143; 214pp; English.
XX

CC The present invention describes a composition comprising a prepared
CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
CC These are derived from HCV HLA-binding motifs. They are useful in
CC vaccines for the prevention and treatment of HCV infection in humans. The
CC present sequence is an epitope used in the disclosure of the invention.
XX
SQ Sequence 8 AA;

Query Match 2.1%; Score 6; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 145 SPQGRV 150
|||||
DB 1 spqgrv 6

RESULT 4

AAJ47926
ID AAJ47926 standard; Peptide; 9 AA.

XX AC AAJ47926;

XX DT 01-DEC-1999 (first entry)

XX DE Immunogenic peptide having a human leukocyte antigen binding motif #2537.

XX KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
KW Immune response; T cell activation; major histocompatibility complex;

KM cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
 KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
 KW vaccine; immunisation.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9945954-A1.
 XX
 PD 16-SEP-1999.
 XX
 PF 13-MAR-1998; 98WO-US05039.
 XX
 PR 13-MAR-1998; 98WO-US05039.
 XX
 PA (EPTM) EPTMONE INC.
 XX
 PI Sette A, Kubo RT, Sidney J, Cells E, Grey HM, Southwood S;
 XX
 DR WPI; 1999-551214/46.
 XX
 PT New immunogenic peptides with HLA binding motif, useful in treatment
 PT and diagnosis of cancers and viral diseases
 XX
 PS Claim 1; Page 128; 150pp; English.
 XX
 CC AAY45300 to AAY48214 represent specifically claimed immunogenic peptides
 CC having a human major histocompatibility complex (MHC) Class I (also
 CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic
 CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
 CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
 CC response against the antigen from which the peptide is derived.
 CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
 CC normally induced by an antigen in the form of a peptide fragment bound
 CC to a HLA molecule, rather than the intact foreign antigen itself, and
 CC are particularly important in tumour rejection and in fighting viral
 CC infections. The peptides are therefore useful therapeutically to treat
 CC or prevent viral infections and cancers in mammals (especially humans)
 CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
 CC They can be administered as vaccines to elicit an immune response in
 CC individuals susceptible or otherwise at risk of viral infection or
 CC cancer, or used to treat chronic or acute conditions. They are also
 CC useful diagnostically, and can be used to induce a cytotoxic T cell
 CC response, by contacting a cytotoxic T cell with the peptide e.g. to
 CC produce CTLs ex vivo for infusion back into a patient. The
 CC polypeptides encoding the immunogenic peptides are also useful
 CC therapeutically and for immunisation as above.
 CC
 CC Sequence 9 AA;
 SQ

Query Match 2.1%; Score 6; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 145 SPGORV 150
 DB 1 spgqr 6

RESULT 5
 AAB98703
 ID AAB98703 standard; peptide; 9 AA.
 XX
 AC AAB98703;
 XX
 DT 02-AUG-2001 (first entry)
 XX
 DE Cytotoxic T lymphocyte epitopic peptide p214K9 from hepatitis C virus.
 XX
 KW Cytotoxic T lymphocyte epitopic peptide p214K9; hepatitis C virus;
 KW NS3; NS4; NS5a; p214K9; immune response; CTL; HCV;
 KW hepatitis C virus infection.

XX
 OS Hepatitis C virus.
 XX
 PN WO200130812-A2.
 XX
 PD 03-MAY-2001.
 XX
 PF 27-OCT-2000; 2000WO-US29594.
 XX
 PR 27-OCT-1999; 99US-0161713.
 XX
 PA (CHIR) CHIRON CORP.
 XX
 PI Pallard X, Houghton M, Selby M;
 XX
 DR WPI; 2001-328648/34.
 XX
 PT Hepatitis C virus (HCV) polypeptides and fusion proteins, useful for
 PT stimulating cell-mediated immune responses, particularly for
 PT therapeutic or prophylactic treatment against HCV infection hepatitis C
 PT virus.
 XX
 PS Claim 31; Page 15; 56pp; English.
 XX
 CC The present sequence represents cytotoxic T lymphocyte epitopic peptide
 CC p214K9 which comes from hepatitis C virus NS5a protein (HCV-NS5a), this
 CC sequence was used in an experiment of the invention to show that
 CC immunisation with plasmid or naked DNA encoding an NS3NS4NS5a fusion
 CC protein will activate CD8+ cells which recognise and lyse target cells
 CC displaying an NS5a epitope. The present sequence was useful in the
 CC production of the invention which includes fusion proteins comprising
 CC either an NS3, NS4 and NS5a polypeptide of HCV, or an NS3, NS4, NS5a and
 CC NS5b polypeptide of an HCV. The HCV polypeptides are particularly useful
 CC for stimulating cell-mediated immune responses, e.g. activating
 CC HCV-specific T cells. The fusion protein is useful for generating an
 CC immune response against HCV in a mammal, particularly a cytotoxic T
 CC lymphocyte (CTL) response for either therapeutic or prophylactic
 CC treatment against HCV infection.
 CC
 CC Sequence 9 AA;
 SQ

Query Match 2.1%; Score 6; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 46 EYPVGS 51
 DB 2 eyvgs 7

RESULT 6
 AAJ00162
 ID AAJ00162 standard; peptide; 9 AA.
 XX
 AC AAJ00162;
 XX
 DT 02-JUL-2001 (first entry)
 XX
 DE Hepatitis C virus epitope #153.
 XX
 KW Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 KW antiviral.
 XX
 OS Hepatitis C virus.
 XX
 PN WO200121189-A1.
 XX
 PD 29-MAR-2001.
 XX
 DE 19-JUL-2000; 2000WO-US19774.
 XX
 PR 19-JUL-1999; 99US-0357737.

XX (EPIM-) EPIMMUNE INC.
 XX
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Cells E, Kubo RT, Grey HM;
 XX
 XX WPI; 2001-308046/32.
 DR
 XX
 PT A new composition useful as a vaccines against hepatitis C virus
 PS
 PS Disclosure: Page 104; 214pp; English.
 XX
 XX The present invention describes a composition comprising a prepared
 CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in
 CC vaccines for the prevention and treatment of HCV infection in humans. The
 CC present sequence is an epitope used in the disclosure of the invention.
 XX
 SQ Sequence 9 AA;

Query Match 2.1%; Score 6; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 145 SPQGRV 150
 |||||
 DB 2 spqgrv 7

RESULT 7
 AAJ00288
 ID AAJ00288 standard; Peptide; 9 AA.
 XX
 AC AAJ00288;
 XX
 DT 02-JUL-2001 (first entry)
 XX
 DE Hepatitis C virus epitope #279.
 XX
 DE Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 KM antiviral.
 KM
 OS Hepatitis C virus;
 XX
 PN WO200121189-A1.
 XX
 PD 29-MAR-2001.
 XX
 PF 19-JUL-2000; 2000WO-US19774.
 XX
 PR 19-JUL-1999; 99US-0357737.
 XX
 PA (EPIM-) EPIMMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Cells E, Kubo RT, Grey HM;
 XX
 DR WPI; 2001-308046/32.
 XX
 PT A new composition useful as a vaccines against hepatitis C virus
 PS
 PS Disclosure: Page 107; 214pp; English.
 XX
 XX The present invention describes a composition comprising a prepared
 CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in
 CC vaccines for the prevention and treatment of HCV infection in humans. The
 CC present sequence is an epitope used in the disclosure of the invention.
 XX
 SQ Sequence 9 AA;

Query Match 2.1%; Score 6; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 145 SPQGRV 150
 |||||
 DB 4 spqgrv 9

RESULT 8
 AAJ01152
 ID AAJ01152 standard; Peptide; 9 AA.
 XX
 AC AAJ01152;
 XX
 DT 02-JUL-2001 (first entry)
 XX
 DE Hepatitis C virus epitope #1143.
 XX
 DE Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 KM antiviral.
 KM
 OS Hepatitis C virus.
 XX
 PN WO200121189-A1.
 XX
 PD 29-MAR-2001.
 XX
 PF 19-JUL-2000; 2000WO-US19774.
 XX
 PR 19-JUL-1999; 99US-0357737.
 XX
 PA (EPIM-) EPIMMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Cells E, Kubo RT, Grey HM;
 XX
 DR WPI; 2001-308046/32.
 XX
 PT A new composition useful as a vaccines against hepatitis C virus
 PS
 PS Disclosure: Page 129; 214pp; English.
 XX
 CC The present invention describes a composition comprising a prepared
 CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
 CC These are derived from HCV HLA-binding motifs. They are useful in
 CC vaccines for the prevention and treatment of HCV infection in humans. The
 CC present sequence is an epitope used in the disclosure of the invention.
 XX
 SQ Sequence 9 AA;

Query Match 2.1%; Score 6; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 4.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 145 SPQGRV 150
 |||||
 DB 1 spqgrv 6

RESULT 9
 AAJ01463
 ID AAJ01463 standard; Peptide; 9 AA.
 XX
 AC AAJ01463;
 XX
 DT 02-JUL-2001 (first entry)
 XX
 DE Hepatitis C virus epitope #1454.
 XX
 DE Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
 KM antiviral.
 KM

XX Hepatitis C virus.
OS
XX WO200121189-A1.
PN
XX
XX 29-MAR-2001.
PD
XX
XX 19-JUL-2000; 2000WO-US19774.
PF
XX
XX 19-JUL-1999; 99US-0357737.
PR
XX
XX (EPIIM-) EPIMMUNE INC.
PA
XX
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
PI
XX WPI: 2001-308046/32.
DR
XX
XX A new composition useful as a vaccines against hepatitis C virus
PT
XX
XX Disclosure: Page 137; 214pp; English.
PS
XX
XX The present invention describes a composition comprising a prepared
CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
CC These are derived from HCV HLA-binding motifs. They are useful in
CC vaccines for the prevention and treatment of HCV infection in humans. The
CC present sequence is an epitope used in the disclosure of the invention.
CC
XX
XX Sequence 9 AA;
SQ

Query Match 2.1%; Score 6; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.3e+05; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;
OY 145 SPQGRV 150
DB 2 spqgrv 7

RESULT 10
AAJ01758
ID AAJ01758 standard; Peptide: 9 AA.
XX
XX AAJ01758;
AC
XX 02-JUL-2001 (first entry)
DT
XX
XX Hepatitis C virus epitope #1749.
DE
XX
XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
KM antiviral.
KM
XX
XX Hepatitis C virus.
OS
XX
XX WO200121189-A1.
PN
XX
XX 29-MAR-2001.
PD
XX
XX 19-JUL-2000; 2000WO-US19774.
PF
XX
XX 19-JUL-1999; 99US-0357737.
PR
XX
XX (EPIIM-) EPIMMUNE INC.
PA
XX
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
PI
XX WPI: 2001-308046/32.
DR
XX
XX A new composition useful as a vaccines against hepatitis C virus
PT
XX
XX Disclosure: Page 144; 214pp; English.
PS

XX The present invention describes a composition comprising a prepared
CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
CC These are derived from HCV HLA-binding motifs. They are useful in
CC vaccines for the prevention and treatment of HCV infection in humans. The
CC present sequence is an epitope used in the disclosure of the invention.
CC
XX
XX Sequence 9 AA;
SQ

Query Match 2.1%; Score 6; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.3e+05; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;
OY 145 SPQGRV 150
DB 4 spqgrv 9

RESULT 11
AAJ01819
ID AAJ01819 standard; Peptide: 9 AA.
XX
XX AAJ01819;
AC
XX 02-JUL-2001 (first entry)
DT
XX
XX Hepatitis C virus epitope #1810.
DE
XX
XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
KM antiviral.
KM
XX
XX Hepatitis C virus.
OS
XX
XX WO200121189-A1.
PN
XX
XX 29-MAR-2001.
PD
XX
XX 19-JUL-2000; 2000WO-US19774.
PF
XX
XX 19-JUL-1999; 99US-0357737.
PR
XX
XX (EPIIM-) EPIMMUNE INC.
PA
XX
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
PI
XX WPI: 2001-308046/32.
DR
XX
XX A new composition useful as a vaccines against hepatitis C virus
PT
XX
XX Disclosure: Page 145; 214pp; English.
PS
XX
XX The present invention describes a composition comprising a prepared
CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
CC These are derived from HCV HLA-binding motifs. They are useful in
CC vaccines for the prevention and treatment of HCV infection in humans. The
CC present sequence is an epitope used in the disclosure of the invention.
CC
XX
XX Sequence 9 AA;
SQ

Query Match 2.1%; Score 6; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.3e+05; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0;
OY 145 SPQGRV 150
DB 1 spqgrv 6

RESULT 12
AAJ02614

ID AAJ02614 standard; Peptide; 9 AA.
XX
XX AAJ02614;
AC
XX
XX 02-JUL-2001 (first entry)
DT
XX
XX Hepatitis C virus epitope #2605.
DE
XX
XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
KM antiviral.
XX
XX Hepatitis C virus.
OS
XX WO200121189-A1.
PN
XX
XX 29-MAR-2001.
PD
XX
XX 19-JUL-2000; 2000WO-US19774.
PF
XX
XX 19-JUL-1999; 99US-0357737.
PR
XX
XX (EPIM-) EPIMMUNE INC.
PA
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Cells E, Kubo RT, Grey HM;
XX
XX WPI; 2001-308046/32.
DR
XX
XX A new composition useful as a vaccine against hepatitis C virus -
PT
XX
XX Disclosure; Page 164; 214pp; English.
PS
XX
XX The present invention describes a composition comprising a prepared
CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
CC These are derived from HCV HLA-binding motifs. They are useful in
CC vaccines for the prevention and treatment of HCV infection in humans. The
CC present sequence is an epitope used in the disclosure of the invention.
CQ
XX
XX Sequence 9 AA;

Query Match 2.1%; Score 6; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 145 SPCQRY 150
IIIIII
DB 2 spqqr 7

RESULT 13
AAJ03766
ID AAJ03766 standard; Peptide; 9 AA.
XX
XX AAJ03766;
AC
XX
XX 02-JUL-2001 (first entry)
DT
XX
XX Hepatitis C virus epitope #3757.
DE
XX
XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
KM antiviral.
XX
XX Hepatitis C virus.
OS
XX WO200121189-A1.
PN
XX
XX 29-MAR-2001.
PD
XX
XX 19-JUL-2000; 2000WO-US19774.
PF
XX
XX 19-JUL-1999; 99US-0357737.
PR
XX
XX

PA (EPIM-) EPIMMUNE INC.
XX
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Cells E, Kubo RT, Grey HM;
XX
XX WPI; 2001-308046/32.
DR
XX
XX A new composition useful as a vaccine against hepatitis C virus -
PT
XX
XX Disclosure; Page 185; 214pp; English.
PS
XX
XX The present invention describes a composition comprising a prepared
CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
CC These are derived from HCV HLA-binding motifs. They are useful in
CC vaccines for the prevention and treatment of HCV infection in humans. The
CC present sequence is an epitope used in the disclosure of the invention.
CQ
XX
XX Sequence 9 AA;

Query Match 2.1%; Score 6; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 145 SPCQRY 150
IIIIII
DB 1 spqqr 6

RESULT 14
AAJ03901
ID AAJ03901 standard; Peptide; 9 AA.
XX
XX AAJ03901;
AC
XX
XX 02-JUL-2001 (first entry)
DT
XX
XX Hepatitis C virus epitope #3892.
DE
XX
XX Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
KM antiviral.
XX
XX Hepatitis C virus.
OS
XX WO200121189-A1.
PN
XX
XX 29-MAR-2001.
PD
XX
XX 19-JUL-2000; 2000WO-US19774.
PF
XX
XX 19-JUL-1999; 99US-0357737.
PR
XX
XX (EPIM-) EPIMMUNE INC.
PA
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Cells E, Kubo RT, Grey HM;
XX
XX WPI; 2001-308046/32.
DR
XX
XX A new composition useful as a vaccine against hepatitis C virus -
PT
XX
XX Example 2; Page 193; 214pp; English.
PS
XX
XX The present invention describes a composition comprising a prepared
CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
CC These are derived from HCV HLA-binding motifs. They are useful in
CC vaccines for the prevention and treatment of HCV infection in humans. The
CC present sequence is an epitope used in the disclosure of the invention.
CQ
XX
XX Sequence 9 AA;

Query Match 2.1%; Score 6; DB 22; Length 9;

Best Local Similarity 100.0%; Pred. No. 4.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 145 SPQGRV 150
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DB 1 spqgrv 6

DB 3 vqrkrg 8

Search completed: January 24, 2002, 16:25:45
Job time: 130 sec

RESULT 15

AAI49753
ID AAY49753 standard; peptide; 10 AA.

AC AAY49753;

DT 19-JAN-2000 (first entry)

DE Compact structure forming exemplification peptide #46.

KM Compact structure forming peptide; dimerisation; stability; scaffold;
XX library screening; drug screening; gene therapy.

OS Synthetic.

PN WO9951625-A2.

PD 14-OCT-1999.

PF 02-APR-1999; 99WO-US07374.

PR 02-APR-1998; 98US-0080444.

PA (RIGE-) RIGEL PHARM INC.

PI Anderson D;

DR WPI: 1999-620191/53.

PT Novel dimerization peptides which self-associate are used with other
XX proteins to effect the formation of compact structures -

PS Disclosure: Page 18; 75pp; English.

CC The present invention describes peptides which have a moderate or high
CC affinity for each other, when added as extensions to both the N-terminus
CC and C-terminus of a protein, can be used to help fold the protein into
CC a compact structure. This compact structure is more stable to proteases.
CC A composition (A) comprises at least a first dimerisation peptide (I)
CC comprising the sequence (SI) that is no more than 8 amino acids long,
CC where the composition optionally comprises a second dimerisation peptide
CC (II): NH₂-X1-X2-X3-X4-X5-COOH (SI) where X1 to X4 = Ala, Val, Ile, Leu,
CC Trp, Phe, Met, or Tyr, and X5 = Lys, Arg, Asp or Glu;
CC NH₂-X1-X2-X3-X4-X5-COOH (II). The compositions of the invention are
CC displayed intracellularly or extracellularly and are useful to identify
CC binding proteins and molecules, and to modulate intracellular signalling
CC pathways. A library of constrained proteins may be evaluated in vivo for
CC its bioactive potential. The invention can be used to access molecules
CC or targets within living cells, and then provide for the isolation of
CC the constrained protein which has a phenotypic effect on the living
CC cells. The methods are also useful to identify in vitro binding partners
CC of the constrained protein. The compositions of the invention are useful
CC as a scaffold for gene therapy and for potential use as a therapeutic
CC in physiological fluids. The present sequence is used in the
CC exemplification of the present invention.

SQ Sequence 10 AA;

Query Match 2.1%; Score 6; DB 20; Length 10;

Best Local Similarity 100.0%; Pred. No. 79;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 241 YORRRO 246
|||||

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 24, 2002, 16:23:35 ; Search time 12.55 Seconds
(without alignments)
507.445 Million cell updates/sec

Title: US-08-741-095B-26

Perfect score: 283
Sequence: 1 MEPPGDMGPPPPRSTPTDY.....VTVVAVETIPSTGRSPNH 283

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 212252 seqs, 22503292 residues

Word size : 0

Total number of hits satisfying chosen parameters: 132412

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Listing first 45 summaries

Database :

Issued_Patents_AA:*
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3: /cgn2.6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2.6/ptodata/2/1aa/6B.COMB.pep:*
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6: /cgn2.6/ptodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	2.1	10	3	US-09-007-020-3
2	6	2.1	10	4	US-08-789-333F-9
3	6	2.1	10	4	US-09-169-015-19
4	6	2.1	10	4	US-09-133-944-9
5	6	2.1	11	6	5204326-81
6	6	2.1	12	6	5204326-82
7	6	2.1	14	1	US-07-818-781A-1
8	6	2.1	14	1	US-07-817-916A-1
9	6	2.1	14	1	US-08-003-839-1
10	6	2.1	14	5	PCT-US93-06278-1
11	6	2.1	14	6	5204326-83
12	6	2.1	15	6	5204326-84
13	6	2.1	15	6	5204326-89
14	6	2.1	16	6	5204326-85
15	6	2.1	17	5	PCT-US95-13841-2
16	6	2.1	17	6	5204326-86
17	6	2.1	18	6	5204326-87
18	6	2.1	19	6	5204326-80
19	6	2.1	21	6	5204326-88
20	6	2.1	22	6	5204326-91
21	6	2.1	26	1	US-08-595-559-5
22	6	2.1	26	2	US-08-928-958-5
23	6	2.1	26	2	US-09-072-429-5
24	6	2.1	27	2	US-08-392-816-9
25	6	2.1	7	1	US-08-132-164-1
26	5	1.8	7	1	US-08-098-142A-8
27	5	1.8	7	4	US-09-173-941-16

28	5	1.8	7	4	US-09-258-754-429	Sequence 429, App
29	5	1.8	7	4	US-09-042-107-429	Sequence 429, App
30	5	1.8	7	5	PCT-US94-01840-9	Sequence 9, Appli
31	5	1.8	8	4	US-08-444-818-670	Sequence 670, App
32	5	1.8	8	4	US-09-139-802-4	Sequence 4, Appli
33	5	1.8	9	1	US-07-942-245-503	Sequence 503, App
34	5	1.8	9	1	US-08-363-691-4	Sequence 6, Appli
35	5	1.8	9	1	US-08-363-691-6	Sequence 4, Appli
36	5	1.8	9	2	US-08-340-283-184	Sequence 184, App
37	5	1.8	9	2	US-08-104-165-19	Sequence 19, Appli
38	5	1.8	9	3	US-08-464-250-19	Sequence 19, Appli
39	5	1.8	9	4	US-08-464-250-19	Sequence 19, Appli
40	5	1.8	9	4	PCT-US95-02121-90	Sequence 90, Appli
41	5	1.8	9	5	PCT-US95-02121-149	Sequence 149, App
42	5	1.8	10	1	US-08-212-190A-10	Sequence 10, Appli
43	5	1.8	10	2	US-08-900-321-10	Sequence 10, Appli
44	5	1.8	10	5	PCT-US95-03610-10	Sequence 10, Appli
45	5	1.8	11	1	US-07-794-288D-205	Sequence 205, App

ALIGNMENTS

```

RESULT 1
US-09-007-020-3
; Sequence 3, Application US/09007020
; Patent No. 6090539
; GENERAL INFORMATION:
; APPLICANT: Haaf, Thomas
; APPLICANT: Ilya Golub, Efim
; APPLICANT: Reddy, Gurucharan
; APPLICANT: Redding, Charles M.
; APPLICANT: Ward, David C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS UTILIZING RAD51
; FILE REFERENCE: A-65680/RFT/RMS
; CURRENT FILING DATE: 1998-01-14
; EARLIER APPLICATION NUMBER: 60/035,834
; EARLIER FILING DATE: 1997-01-30
; EARLIER APPLICATION NUMBER: 60/045,668
; EARLIER FILING DATE: 1997-05-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentlin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-007-020-3

Query Match          2.1%; Score 6; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 241 YOKRQ 246
   |||||
Db 3 YOKRQ 8

RESULT 2
US-08-789-333F-9
; Sequence 9, Application US/08789333F
; Patent No. 6153380
; GENERAL INFORMATION:
; APPLICANT: Rothenberg, S. M.
; APPLICANT: Rothenberg, Garry P
; TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRACELLULAR
; TITLE OF INVENTION: EFFECTOR PEPTIDES AND RNA MOLECULES
; FILE REFERENCE: A642601DIBRMSDS
; CURRENT APPLICATION NUMBER: US/08/789,333F
; CURRENT FILING DATE: 1997-01-23

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PRIOR APPLICATION NUMBER: 08/589,108
PRIOR FILING DATE: 1996-01-23
PRIOR APPLICATION NUMBER: 08/589,911
PRIOR FILING DATE: 1996-01-23
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO: 9
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: nuclear
OTHER INFORMATION: Localization sequence.
US-08-789-333F-9

Query Match 2.1%; Score 6; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 241 VORRQ 246
DB 3 VORRQ 8

RESULT 3
US-09-169-015-19
Sequence 19, Application US/09169015
Patent No. 6180343
GENERAL INFORMATION:
APPLICANT: Anderson, David
INVENTOR: Bogenberger, Jakob M.
TITLE OF INVENTION: Green Fluorescent Protein Fusions with Random Peptides
FILE REFERENCE: A66900/DJB/RMS/SJR
CURRENT APPLICATION NUMBER: US/09/169,015
CURRENT FILING DATE: 1998-10-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO: 19
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
JOURNAL: Cell
ISSUE: 64
PAGES: 961-
DATE: 1990
US-09-169-015-19

Query Match 2.1%; Score 6; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 241 VORRQ 246
DB 3 VORRQ 8

RESULT 4
US-09-133-944-9
Sequence 9, Application US/09133944
Patent No. 6280937
GENERAL INFORMATION:
APPLICANT: Luo, Ying
APPLICANT: Yu, Pei Wen
APPLICANT: Lorens, James
TITLE OF INVENTION: SHUTTLE VECTORS
FILE REFERENCE: A66252/DJB/DAV
CURRENT APPLICATION NUMBER: US/09/133,944
CURRENT FILING DATE: 1999-08-14
EARLIER APPLICATION NUMBER: 09/133,949
EARLIER FILING DATE: 1998-08-14

NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO: 9
LENGTH: 10
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: NLS
PUBLICATION INFORMATION:
AUTHORS: Ghosh et al.,
JOURNAL: Cell
VOLUME: 62
PAGES: 1019-1019
DATE: 1990
US-09-133-944-9

Query Match 2.1%; Score 6; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 241 VORRQ 246
DB 3 VORRQ 8

RESULT 5
5204326-81
Patent No. 5204326
APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO
INVENTOR: MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,
MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO
TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
METABOLISM IMPROVING AGENT
NUMBER OF SEQUENCES: 147
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/493,359
FILING DATE: 14-MAR-1990
SEQ ID NO: 81
LENGTH: 11
5204326-81

Query Match 2.1%; Score 6; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 TPRTDV 20
DB 1 TPRTDV 6

RESULT 6
5204326-82
Patent No. 5204326
APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO
INVENTOR: INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,
MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO
TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
METABOLISM IMPROVING AGENT
NUMBER OF SEQUENCES: 147
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/493,359
FILING DATE: 14-MAR-1990
SEQ ID NO: 82
LENGTH: 12
5204326-82

Query Match 2.1%; Score 6; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 TPRTDV 20
|||||
Db 2 TPRTDV 7

RESULT 7

US-07-818-781A-1
; Sequence 1, Application US/07818781A
; Patent No. 5231026
; GENERAL INFORMATION:
; APPLICANT: Chang, Tse Wen
; TITLE OF INVENTION: DNA encoding antibodies to antigenic epitopes present on B cell
; TITLE OF INVENTION: basophil surface
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Tanox Biosystems, Inc.
; STREET: 10301 Stella Link Rd.
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: DOS 3.30
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/818,781A
; FILING DATE: 19920106
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: 07/272,243
; FILING DATE: 11/16/1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirabel, Eric P.
; REGISTRATION NUMBER: 31,211
; REFERENCE/DOCKET NUMBER: TNX88-03CCD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 664-2288
; TELEFAX: (713) 664-8914
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; US-07-818-781A-1

Query Match 2.1%; Score 6; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 247 EAEGER 252
|||||

Db 8 EAEGER 13

RESULT 8

US-07-817-916A-1
; Sequence 1, Application US/07817916A
; Patent No. 5252467
; GENERAL INFORMATION:
; APPLICANT: Chang, Tse Wen
; TITLE OF INVENTION: Making antibodies to antigenic epitopes present on B cell but
; TITLE OF INVENTION: surface
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Tanox Biosystems, Inc.
; STREET: 10301 Stella Link Rd.
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77025

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: DOS 3.30
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/817,916A
; FILING DATE: 19920106
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/272,243
; FILING DATE: 11/16/1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirabel, Eric P.
; REGISTRATION NUMBER: 31,211
; REFERENCE/DOCKET NUMBER: TNX88-03BBC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 664-2288
; TELEFAX: (713) 664-8914
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; US-07-817-916A-1

Query Match 2.1%; Score 6; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 247 EAEGER 252
|||||

Db 8 EAEGER 13

RESULT 9

US-08-003-839-1
; Sequence 1, Application US/08003839
; Patent No. 5292867
; GENERAL INFORMATION:
; APPLICANT: Chang, Tse Wen
; TITLE OF INVENTION: Peptides representing antigenic epitopes present on B cell
; TITLE OF INVENTION: surface
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Tanox Biosystems, Inc.
; STREET: 10301 Stella Link Rd.
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: DOS 3.30
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/003,839
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/817,918
; FILING DATE: 1/6/92
; APPLICATION NUMBER: 07/272,243
; FILING DATE: 11/16/1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirabel, Eric P.
; REGISTRATION NUMBER: 31,211
; REFERENCE/DOCKET NUMBER: TNX88-03BBB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 664-2288
; TELEFAX: (713) 664-8914

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-003-839-1

Query Match 2.1%; Score 6; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 247 EAEGEA 252
|||||
DB 8 EAEGEA 13

RESULT 10
PCT-US93-06278-1
Sequence 1, Application PC/TUS9306278
GENERAL INFORMATION:

APPLICANT: Chang, Tse Wen
TITLE OF INVENTION: PEPTIDES REPRESENTING ANTIGENIC EPITOPES OF I9E
TITLE OF INVENTION: PRESENT ON B CELL BUT NOT BASOPHIL SURFACE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Tanox Biosystems, Inc.
STREET: 10301 Stella Link Rd.
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77025

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch
OPERATING SYSTEM: DOS 3.30
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06278
FILING DATE: 19930701
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/468,766
FILING DATE: 01/23/1990
ATTORNEY/AGENT INFORMATION:
NAME: Mirabel, Eric P.

REGISTRATION NUMBER: 31,211
REFERENCE/DOCKET NUMBER: TNX88-03DDE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 664-2288
TELEFAX: (713) 664-8914
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
PCT-US93-06278-1

Query Match 2.1%; Score 6; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 247 EAEGEA 252
|||||
DB 8 EAEGEA 13

RESULT 11
5204326-83
Patent No. 5204326
APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO
; INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,

;MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO
; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM

; METABOLISM IMPROVING AGENT
; NUMBER OF SEQUENCES: 147
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/493,359
; FILING DATE: 14-MAR-1990
; SEQ ID NO:83:
; LENGTH: 14
5204326-83

Query Match 2.1%; Score 6; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 TPRTDV 20
|||||
DB 4 TPRTDV 9

RESULT 12
5204326-84
Patent No. 5204326
APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO
; INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,
;MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO
; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
; METABOLISM IMPROVING AGENT
; NUMBER OF SEQUENCES: 147
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/493,359
; FILING DATE: 14-MAR-1990
; SEQ ID NO:84:
; LENGTH: 15
5204326-84

Query Match 2.1%; Score 6; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 TPRTDV 20
|||||
DB 5 TPRTDV 10

RESULT 13
5204326-89
Patent No. 5204326
APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIHITO;SHIMIZU, FUMIO
; INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,
;MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO
; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
; METABOLISM IMPROVING AGENT
; NUMBER OF SEQUENCES: 147
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/493,359
; FILING DATE: 14-MAR-1990
; SEQ ID NO:89:
; LENGTH: 15
5204326-89

Query Match 2.1%; Score 6; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 TPRTDV 20
|||||
DB 5 TPRTDV 10

RESULT 14
5204326-85
; Patent No. 5204326
; APPLICANT: FUJII, SETSURO;YAMAMOTO, YOSHIIITO;SHIMIZU, FUMIO
; INAI, MASATOSHI;KINOSHITA, NAOSUMI;NAKAMURA, SHIZUO;HIROHASHI,
; MITSURU; SAKAMOTO, TAKASHI;TSUTSUMI, KAZUHIKO;SHIRASAKA, TETSUHIKO
; TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
; METABOLISM IMPROVING AGENT
; NUMBER OF SEQUENCES: 147
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/493,359
; FILING DATE: 14-MAR-1990
; SEQ ID NO:85:
; LENGTH: 16
5204326-85

Query Match 2.1%; Score 6; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 TPRTDV 20
|||||
DB 6 TPRTDV 11

RESULT 15
PCT-US95-13841-2
; Sequence 2, Application PC/TUS9513841
; GENERAL INFORMATION:
; APPLICANT: United Biomedical Inc; Walfield, Alan M.;
; APPLICANT: Wang, Chang xi
; TITLE OF INVENTION: Synthetic Ige Membrane Anchor
; TITLE OF INVENTION: Peptide Immunogens for the Treatment of Allergy
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/13841
; FILING DATE: 25-OCT-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/328,519
; FILING DATE: 25-OCT-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lin, Maria C.H.
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4117
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US95-13841-2

Query Match 2.1%; Score 6; DB 5; Length 17;

Best Local Similarity 100.0%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 247 EAEGEA 252
|||||
DB 9 EAEGEA 14

Search completed: January 24, 2002, 16:26:05
Job time: 150 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 24, 2002, 16:25:05 ; Search time 95.71 Seconds
(without alignments)
820.990 Million cell updates/sec

Title: US-08-741-095b-26

Perfect score: 283

Sequence: 1 MEPPGDWGPMPMRSTPTDY.....VTVAVEETIPSTGRSPNH 283

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 3148936 seqs, 27657034 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105503

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Listing first 45 summaries

Database : Pending_Patents_AA_Main:*

1: /cgn2_6/ptodata/2/paa/PCYUS_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US080_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US081_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US082_COMB.pep:*
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23: /cgn2_6/ptodata/2/paa/US099_COMB.pep:*
24: /cgn2_6/ptodata/2/paa/US099_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	8.8	25	1	PCT-US99-20180-51
2	25	8.8	25	17	US-09-342-767-51
3	22	7.8	22	1	PCT-US99-20180-50
4	22	7.8	22	17	US-09-342-767-50
5	15	5.3	15	14	US-09-086-582-21
6	7	2.5	25	14	US-09-724-059-21780
7	7	2.5	25	21	US-09-724-059-34140
8	6	2.1	8	17	US-09-357-737-1066
9	6	2.1	8	17	US-09-357-737-1617

10	6	2.1	8	17	US-09-357-737A-1066	Sequence 1066, Ap
11	6	2.1	8	17	US-09-357-737A-1617	Sequence 1617, Ap
12	6	2.1	8	17	US-09-357-737B-1066	Sequence 1066, Ap
13	6	2.1	8	17	US-09-357-737B-1617	Sequence 1617, Ap
14	6	2.1	8	17	PCT-US00-23913-82	Sequence 82, Appl
15	6	2.1	9	6	US-08-278-634-90	Sequence 90, Appl
16	6	2.1	9	6	US-08-344-824-101	Sequence 101, Ap
17	6	2.1	9	7	US-08-344-824A-95	Sequence 95, Appl
18	6	2.1	9	14	US-09-017-743A-82	Sequence 82, Appl
19	6	2.1	9	14	US-09-017-743C-82	Sequence 82, Appl
20	6	2.1	9	17	US-09-357-737-77	Sequence 77, Appl
21	6	2.1	9	17	US-09-357-737-203	Sequence 203, Appl
22	6	2.1	9	17	US-09-357-737-1067	Sequence 1067, Ap
23	6	2.1	9	17	US-09-357-737-1378	Sequence 1378, Ap
24	6	2.1	9	17	US-09-357-737-1673	Sequence 1673, Ap
25	6	2.1	9	17	US-09-357-737-1734	Sequence 1734, Ap
26	6	2.1	9	17	US-09-357-737-2529	Sequence 2529, Ap
27	6	2.1	9	17	US-09-357-737-3387	Sequence 3387, Ap
28	6	2.1	9	17	US-09-357-737-3664	Sequence 3664, Ap
29	6	2.1	9	17	US-09-357-737A-77	Sequence 77, Appl
30	6	2.1	9	17	US-09-357-737A-203	Sequence 203, Appl
31	6	2.1	9	17	US-09-357-737A-1067	Sequence 1067, Ap
32	6	2.1	9	17	US-09-357-737A-1378	Sequence 1378, Ap
33	6	2.1	9	17	US-09-357-737A-1673	Sequence 1673, Ap
34	6	2.1	9	17	US-09-357-737A-1734	Sequence 1734, Ap
35	6	2.1	9	17	US-09-357-737A-2529	Sequence 2529, Ap
36	6	2.1	9	17	US-09-357-737A-3387	Sequence 3387, Ap
37	6	2.1	9	17	US-09-357-737A-3664	Sequence 3664, Ap
38	6	2.1	9	17	US-09-357-737B-77	Sequence 77, Appl
39	6	2.1	9	17	US-09-357-737B-203	Sequence 203, Appl
40	6	2.1	9	17	US-09-357-737B-1067	Sequence 1067, Ap
41	6	2.1	9	17	US-09-357-737B-1378	Sequence 1378, Ap
42	6	2.1	9	17	US-09-357-737B-1673	Sequence 1673, Ap
43	6	2.1	9	17	US-09-357-737B-1734	Sequence 1734, Ap
44	6	2.1	9	17	US-09-357-737B-2529	Sequence 2529, Ap
45	6	2.1	9	17	US-60-161-713-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
PCT-US99-20180-51
: Sequence 51, Application PC/US9920180
: GENERAL INFORMATION:
: APPLICANT: Millennium Biotherapeutics, Inc.
: TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
: FILE REFERENCE: 09404/079MO1
: CURRENT APPLICATION NUMBER: PCT/US99/20180
: CURRENT FILING DATE: 1999-09-03
: EARLIER APPLICATION NUMBER: US 09/342,767
: EARLIER FILING DATE: 1999-06-29
: EARLIER APPLICATION NUMBER: US 09/146,950
: EARLIER FILING DATE: 1998-09-03
: NUMBER OF SEQ ID NOS: 58
: SOFTWARE: PastSeq for Windows Version 3.0
: SEQ ID NO 51
: LENGTH: 25
: TYPE: PRT
: ORGANISM: Homo sapiens
PCT-US99-20180-51

Query Match 8.8%; Score 25; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.9e-17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 201 WWWFLSGSLVIVICSTVGLICV 225
DB 1 WWWFLSGSLVIVICSTVGLICV 25

RESULT 2
US-09-342-767-51
; Sequence 51, Application US/09342767
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE
; TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED
; FILE REFERENCE: MBI098-061CPI
; CURRENT APPLICATION NUMBER: US/09/342,767
; CURRENT FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: US 09/146,950
; EARLIER FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 25
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-342-767-51

Query Match 8.8%; Score 25; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.9e-17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 201 WWWWFLSGSLVIVYVCSVGLIICV 225
DB 1 WWWWFLSGSLVIVYVCSVGLIICV 25

RESULT 3
PCT-US99-20180-50
; Sequence 50, Application PC/TUS9920180
; GENERAL INFORMATION:
; APPLICANT: Millennium Biotherapeutics, Inc.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
; FILE REFERENCE: 09404/079M01
; CURRENT APPLICATION NUMBER: PCT/US99/20180
; CURRENT FILING DATE: 1999-09-03
; EARLIER APPLICATION NUMBER: US 09/342,767
; EARLIER FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: US 09/146,950
; EARLIER FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 50
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US99-20180-50

Query Match 7.8%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.6e-14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 165 CPPGTSPNGTLEECOHOTKCS 186
DB 1 CPPGTSPNGTLEECOHOTKCS 22

RESULT 4
US-09-342-767-50
; Sequence 50, Application US/09342767
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE
; TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED
; FILE REFERENCE: MBI098-061CPI
; CURRENT APPLICATION NUMBER: US/09/342,767

; CURRENT FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: US 09/146,950
; EARLIER FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 50
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-342-767-50

Query Match 7.8%; Score 22; DB 17; Length 22;
Best Local Similarity 100.0%; Pred. No. 8.6e-14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 165 CPPGTSPNGTLEECOHOTKCS 186
DB 1 CPPGTSPNGTLEECOHOTKCS 22

RESULT 5
US-09-086-582-21
; Sequence 21, Application US/09086582
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: MOORE, PAUL
; TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR
; TITLE OF INVENTION: RECEPTOR-LIKE PROTEIN 8
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/086,582
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: KENLEY K. HOOVER
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PF368BP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-086-582-21

Query Match 5.3%; Score 15; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.7e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 263 DVTTVAVETIPSFT 277
DB 1 DVTTVAVETIPSFT 15

RESULT 6

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US-09-724-059-21780
: Sequence 21780, Application US/09724059
: GENERAL INFORMATION:
: APPLICANT: Choo, Yen
: APPLICANT: Klug, Aaron
: APPLICANT: Isalan, Mark
: TITLE OF INVENTION: Nucleic Acid Binding Proteins
: FILE REFERENCE: P2500USM
: CURRENT APPLICATION NUMBER: US/09/724,059
: CURRENT FILING DATE: 2000-11-28
: PRIOR APPLICATION NUMBER: GB9710809.6
: PRIOR FILING DATE: 1997-05-23
: NUMBER OF SEQ ID NOS: 1407122
: SOFTWARE: Macallilister
: SEQ ID NO 21780
: LENGTH: 25
: TYPE: PRT
: ORGANISM: Artificial sequence
: FEATURE:
: OTHER INFORMATION: Polypeptide sequence
US-09-724-059-21780

Query Match          2.5%; Score 7; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 RTDVLR 23
      |||||
      14 RTDVLR 20

RESULT 7
US-09-724-059-34140
: Sequence 34140, Application US/09724059
: GENERAL INFORMATION:
: APPLICANT: Choo, Yen
: APPLICANT: Klug, Aaron
: APPLICANT: Isalan, Mark
: TITLE OF INVENTION: Nucleic Acid Binding Proteins
: FILE REFERENCE: P2500USM
: CURRENT APPLICATION NUMBER: US/09/724,059
: CURRENT FILING DATE: 2000-11-28
: PRIOR APPLICATION NUMBER: GB9710809.6
: PRIOR FILING DATE: 1997-05-23
: NUMBER OF SEQ ID NOS: 1407122
: SOFTWARE: Macallilister
: SEQ ID NO 34140
: LENGTH: 25
: TYPE: PRT
: ORGANISM: Artificial sequence
: FEATURE:
: OTHER INFORMATION: Polypeptide sequence
US-09-724-059-34140

Query Match          2.5%; Score 7; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 RTDVLR 23
      |||||
      14 RTDVLR 20

RESULT 8
US-09-357-737-1066
: Sequence 1066, Application US/09357737
: GENERAL INFORMATION:
: APPLICANT: Sette, Alessandro
: APPLICANT: Sidney, John
: APPLICANT: Southwood, Scott
: APPLICANT: Livingston, Brian
: APPLICANT: Livingstone, Brian
```

```
: APPLICANT: Chesnut, Robert
: APPLICANT: Baker, Denise
: APPLICANT: Celis, Esteban
: APPLICANT: Kudo, Ralph
: APPLICANT: Grey, Howard
: TITLE OF INVENTION: INDUCING CELLULAR RESPONSES TO HEPATITIS
: FILE REFERENCE: 18623-014000US
: CURRENT APPLICATION NUMBER: US/09/357,737
: CURRENT FILING DATE: 1999-07-19
: PRIOR APPLICATION NUMBER: U.S.S.N. 09/189,702
: PRIOR FILING DATE: 1998-11-10
: PRIOR APPLICATION NUMBER: U.S.S.N. 08/205,713
: PRIOR FILING DATE: 1994-03-04
: PRIOR APPLICATION NUMBER: U.S.S.N. 08/159,184
: PRIOR FILING DATE: 1993-11-29
: PRIOR APPLICATION NUMBER: U.S.S.N. 08/073,205
: PRIOR FILING DATE: 1993-06-04
: PRIOR APPLICATION NUMBER: U.S.S.N. 08/027,146
: PRIOR FILING DATE: 1993-03-05
: NUMBER OF SEQ ID NOS: 3681
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1066
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Hepatitis C Virus
US-09-357-737-1066

Query Match          2.1%; Score 6; DB 17; Length 8;
Best Local Similarity 100.0%; Pred. No. 2,9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 145 SPGRV 150
      |||||
      1 SPGRV 6

RESULT 9
US-09-357-737-1617
: Sequence 1617, Application US/09357737
: GENERAL INFORMATION:
: APPLICANT: Sette, Alessandro
: APPLICANT: Sidney, John
: APPLICANT: Southwood, Scott
: APPLICANT: Livingston, Brian
: APPLICANT: Chesnut, Robert
: APPLICANT: Baker, Denise
: APPLICANT: Celis, Esteban
: APPLICANT: Kudo, Ralph
: APPLICANT: Grey, Howard
: TITLE OF INVENTION: INDUCING CELLULAR RESPONSES TO HEPATITIS
: FILE REFERENCE: 18623-014000US
: CURRENT APPLICATION NUMBER: US/09/357,737
: CURRENT FILING DATE: 1999-07-19
: PRIOR APPLICATION NUMBER: U.S.S.N. 09/189,702
: PRIOR FILING DATE: 1998-11-10
: PRIOR APPLICATION NUMBER: U.S.S.N. 08/205,713
: PRIOR FILING DATE: 1994-03-04
: PRIOR APPLICATION NUMBER: U.S.S.N. 08/159,184
: PRIOR FILING DATE: 1993-11-29
: PRIOR APPLICATION NUMBER: U.S.S.N. 08/073,205
: PRIOR FILING DATE: 1993-06-04
: PRIOR APPLICATION NUMBER: U.S.S.N. 08/027,146
: PRIOR FILING DATE: 1993-03-05
: NUMBER OF SEQ ID NOS: 3681
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 1617
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Hepatitis C Virus
US-09-357-737-1617
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Query Match	2.1%;	Score 6;	DB 17;	Length 8;
Best Local Similarity	100.0%;	Pred. No. 2.9e+06;		
Matches	6;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;

QY	145	SPGQRV	150
			.
Db	1	SPGQRV	6

RESULT 10
US-09-357-737A-1066
Sequence 1066, Application US/09357737A

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1066
; LENGTH: 8
; TYPE: PRY
; ORGANISM: Hepatitis C Virus
; OS-09-357-737A-1066

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QY      145 SPGQRV 150
        |||||
Db       1 SPGQRV 6
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US-09-357-737A-1617
 : Result 11
 : Sequence 1617, Application US/09357737A
 : GENERAL INFORMATION:
 : APPLICANT: Sette, Alessandro
 : APPLICANT: Sidney, John
 : APPLICANT: Southwood, Scott
 : APPLICANT: Livingston, Brian
 : APPLICANT: Chesnut, Robert
 : APPLICANT: Baker, Denise
 : APPLICANT: Celis, Esteban
 : APPLICANT: Kubo, Ralph
 : APPLICANT: Grey, Howard
 : TITLE OF INVENTION: INDUCING CELLULAR RESPONSES TO HEPATITIS
 : TITLE OF INVENTION: C VIRUS USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
 : FILE REFERENCE: 18623-01400005

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1 CURRENT APPLICATION NUMBER: US/09/357,737A
2 CURRENT FILING DATE: 1999-07-19
3 PRIOR APPLICATION NUMBER: U.S.S.N. 09/189,702
4 PRIOR FILING DATE: 1998-11-10
5 PRIOR APPLICATION NUMBER: U.S.S.N. 08/205,713
6 PRIOR FILING DATE: 1994-03-04
7 PRIOR APPLICATION NUMBER: U.S.S.N. 08/159,184
8 PRIOR FILING DATE: 1993-11-29
9 PRIOR APPLICATION NUMBER: U.S.S.N. 08/073,205
10 PRIOR FILING DATE: 1993-06-04
11 PRIOR APPLICATION NUMBER: U.S.S.N. 08/027,146
12 PRIOR FILING DATE: 1993-03-05
13 NUMBER OF SEQ ID NOS: 3681
14 SOFTWARE: FastSeq for Windows Version 4.0
15 SEQ ID NO 1617
16 LENGTH: 8
17 TYPE: PRT
18 ORGANISM: Hepatitis C Virus
19 US-09-357-737A-1617

```

Query Match	2.1%;	Score 6;	DB 17;	Length 8;
Best Local Similarity	100.0%;	Pred. No. 2.9e+6;		
Matches	6;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;

```
QY      145 SPGQRV 150
          |||||
Db       1 SPGQRV 6
```

```

RESULT 12
US-09-357-737B-1066
Sequence 1066, Application US/09357737B
GENERAL INFORMATION:
APPLICANT: Settle, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
APPLICANT: Baker, Denise
APPLICANT: Celis, Esteban
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard
APPLICANT: Epimmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Hepatitis C
TITLE OF INVENTION: Virus Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 018623-014000US
CURRENT APPLICATION NUMBER: US/09/357,737B
CURRENT FILING DATE: 1999-07-19
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 09/189,702
PRIOR FILING DATE: 1998-11-10
NUMBER OF SEQ ID NOS: 3683
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1066
LENGTH: 8
TYPE: PRT
ORGANISM: Hepatitis C Virus
US-09-357-737B-1066

```

Query Match	2.1%	Score 6;	DB 17;	Length 8;
Best Local Similarity	100.0%	Pred. No. 2.9e+06;		
Matches 6;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Oy	145	SPGORV	150	

QY 145 SPGQRV 150

Db 1 SPQGRV 6
|||||

RESULT 13

US-09-357-737B-1617
; Sequence 1617, Application US/09357737B
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Hepatitis C
; FILE REFERENCE: 018623-014000US
; CURRENT FILING DATE: 1999-07-19
; PRIOR FILING DATE: 1993-03-05
; PRIOR FILING DATE: 1993-03-05
; PRIOR FILING DATE: 1993-03-05
; PRIOR FILING DATE: 1993-06-04
; PRIOR FILING DATE: 1993-11-29
; PRIOR FILING DATE: 1994-03-04
; PRIOR FILING DATE: 1998-11-10
; NUMBER OF SEQ ID NOS: 3683
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1617
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Hepatitis C Virus
US-09-357-737B-1617

Query Match 2.1%; Score 6; DB 17; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 145 SPQGRV 150
|||||

Db 1 SPQGRV 6

RESULT 14

PCT-US00-23913-82
; Sequence 82, Application PC/TUS0023913
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: HLA Binding Peptides and Their Uses
; FILE REFERENCE: 18623-80-5PC
; CURRENT FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 82
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV NS5 2615, peptide 1292.23
PCT-US00-23913-82

Query Match 2.1%; Score 6; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 145 SPQGRV 150
|||||

Db 1 SPQGRV 6

RESULT 15

US-08-278-634-90
; Sequence 90, Application US/08278634
; GENERAL INFORMATION:
; APPLICANT: SETTE, Alessandro
; APPLICANT: SIDNEY, John
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
; NUMBER OF SEQUENCES: 288
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Street Tower, 20th
; STREET: Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/278,634
; FILING DATE: 21-JUL-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/543-9600
; TELEFAX: 415/543-5043
; INFORMATION FOR SEQ ID NO: 90:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-278-634-90

Query Match 2.1%; Score 6; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.9e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 145 SPQGRV 150
|||||

Db 1 SPQGRV 6

Search completed: January 24, 2002, 16:28:09
Job time: 184 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 24, 2002, 16:25:20 ; Search time 13.32 Seconds
(without alignments)
738.763 Million cell updates/sec

Title: US-08-741-095B-26

Perfect score: 283
Sequence: 1 MEPPGDMGPPMRSTPRTDV.....VTIYVVEITIPSTGRSPNH 283

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 160442 seqs, 34771459 residues

Word size: 0

Total number of hits satisfying chosen parameters: 39628

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Listing first 45 summaries

Database: Pending_Patents_AA_New:*

1: /cgn2_6/ptodata/1/paa/PC1_NEW_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6	2.1	10	5	US-09-916-940-9
2	6	2.1	10	5	US-09-572-404B-1338
3	6	2.1	24	4	US-08-816-011E-10
4	6	2.1	24	4	US-08-816-011E-18
5	6	2.1	24	4	US-08-816-011F-10
6	6	2.1	24	4	US-08-816-011F-18
7	6	2.1	7	1	PCT-US01-28124A-17
8	5	1.8	9	5	US-09-881-636-38
9	5	1.8	9	5	US-09-881-636-61
10	5	1.8	9	5	US-09-881-636-128
11	5	1.8	9	5	US-09-881-636-236
12	5	1.8	9	5	US-09-881-636-339
13	5	1.8	9	5	US-09-881-636-426
14	5	1.8	9	5	US-09-881-636-532
15	5	1.8	9	5	US-09-881-636-633
16	5	1.8	9	5	US-09-881-636-660
17	5	1.8	10	4	US-08-816-454B-76
18	5	1.8	10	5	US-09-881-636-104
19	5	1.8	10	5	US-09-881-636-111
20	5	1.8	10	5	US-09-881-636-192
21	5	1.8	10	5	US-09-881-636-507
22	5	1.8	10	5	US-09-881-636-608
23	5	1.8	10	5	US-09-881-636-701
24	5	1.8	10	5	US-09-572-404B-258
25	5	1.8	10	5	US-09-572-404B-727
26	5	1.8	10	5	US-09-572-404B-747

27	5	1.8	10	5	US-09-572-404B-1580	Sequence 1580, Ap
28	5	1.8	10	5	US-09-572-404B-3020	Sequence 3020, Ap
29	5	1.8	10	5	US-09-572-404B-3778	Sequence 3778, Ap
30	5	1.8	10	5	US-09-572-404B-3779	Sequence 3779, Ap
31	5	1.8	13	5	US-09-813-333-54	Sequence 54, Appl
32	5	1.8	13	5	US-09-522-900-52	Sequence 52, Appl
33	5	1.8	13	5	US-09-539-382-52	Sequence 52, Appl
34	5	1.8	13	5	US-09-920-954-11	Sequence 11, Appl
35	5	1.8	13	6	US-10-010-568-31	Sequence 31, Appl
36	5	1.8	18	5	US-09-341-349C-6	Sequence 6, Appl
37	5	1.8	19	5	US-09-974-879-318	Sequence 318, App
38	5	1.8	21	5	US-09-810-428-5	Sequence 5, Appl
39	5	1.8	22	5	US-09-402-181A-284	Sequence 284, App
40	5	1.8	22	5	US-09-721-477-284	Sequence 284, App
41	5	1.8	22	5	US-09-766-253-164	Sequence 164, App
42	5	1.8	22	6	US-10-006-920-331	Sequence 331, App
43	5	1.8	22	6	US-10-010-940-331	Sequence 331, App
44	5	1.8	22	6	US-10-012-896-331	Sequence 331, App
45	5	1.8	23	5	US-09-690-454-107	Sequence 107, App

ALIGNMENTS

```
RESULT 1
US-09-916-940-9
; Sequence 9, Application US/09916940
; GENERAL INFORMATION:
; APPLICANT: Nolan, Gary P
; TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRACELLULAR
; FILE REFERENCE: A-64260-6/RMS/RMS
; CURRENT APPLICATION NUMBER: US/09/916,940
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 09/727,715
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 08/963,368
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: US 08/589,109
; PRIOR FILING DATE: 1996-01-23
; PRIOR APPLICATION NUMBER: US 08/589,911
; PRIOR FILING DATE: 1996-01-23
; PRIOR APPLICATION NUMBER: US 08/789,333
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: US 08/787,738
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: nuclear
US-09-916-940-9
; OTHER INFORMATION: Localization sequence.

Query Match 2.1%; Score 6; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 241 VORKRO 246
Db 3 VORKRO 8

RESULT 2
US-09-572-404B-1338
; Sequence 1338, Application US/09572404B
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
```

```
FILE REFERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProPatent version 1.0
SEQ ID NO 1338
LENGTH: 10
TYPE: PRT
ORGANISM: Homo Sapiens
FEATURE:
OTHER INFORMATION: sequence located in MLL OR HRX OR ALL1 OR TRX1 OR HTRX at 721-730
US-09-572-404B-1338
```

```
Query Match      2.1%; Score 6; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 194 AGTSSS 199
      |||||
Db 4 AGTSSS 9
```

```
RESULT 3
US-08-816-011E-10
; Sequence 10, Application US/08816011E
; GENERAL INFORMATION:
; APPLICANT: Pausch, Mark H
; APPLICANT: Price, Laura A
; TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
; FILE REFERENCE: 01142.0122 SEQUENCE LISTING
; CURRENT APPLICATION NUMBER: US/08/816,011E
; CURRENT FILING DATE: 1997-03-11
; PRIOR APPLICATION NUMBER: 08/332,312
; PRIOR FILING DATE: 1994-10-31
; PRIOR APPLICATION NUMBER: PCT/US95/14364
; PRIOR FILING DATE: 1995-10-25
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 10
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-08-816-011E-10
```

```
Query Match      2.1%; Score 6; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 215 VCSTVG 220
      |||||
Db 8 VCSTVG 13
```

```
RESULT 4
US-08-816-011E-18
; Sequence 18, Application US/08816011E
; GENERAL INFORMATION:
; APPLICANT: Pausch, Mark H
; APPLICANT: Price, Laura A
; TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
; FILE REFERENCE: 01142.0122 SEQUENCE LISTING
; CURRENT APPLICATION NUMBER: US/08/816,011E
; CURRENT FILING DATE: 1997-03-11
; PRIOR APPLICATION NUMBER: 08/332,312
; PRIOR FILING DATE: 1994-10-31
; PRIOR APPLICATION NUMBER: PCT/US95/14364
; PRIOR FILING DATE: 1995-10-25
; NUMBER OF SEQ ID NOS: 67
```

```
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
LENGTH: 24
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-08-816-011E-18
```

```
Query Match      2.1%; Score 6; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 215 VCSTVG 220
      |||||
Db 8 VCSTVG 13
```

```
RESULT 5
US-08-816-011F-10
; Sequence 10, Application US/08816011F
; GENERAL INFORMATION:
; APPLICANT: Pausch, Mark H
; APPLICANT: Price, Laura A
; TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
; FILE REFERENCE: 01142.0122 SEQUENCE LISTING
; CURRENT APPLICATION NUMBER: US/08/816,011F
; CURRENT FILING DATE: 1997-03-11
; PRIOR APPLICATION NUMBER: 08/332,312
; PRIOR FILING DATE: 1994-10-31
; PRIOR APPLICATION NUMBER: PCT/US95/14364
; PRIOR FILING DATE: 1995-10-25
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 10
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-08-816-011F-10
```

```
Query Match      2.1%; Score 6; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 215 VCSTVG 220
      |||||
Db 8 VCSTVG 13
```

```
RESULT 6
US-08-816-011F-18
; Sequence 18, Application US/08816011F
; GENERAL INFORMATION:
; APPLICANT: Pausch, Mark H
; APPLICANT: Price, Laura A
; TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
; FILE REFERENCE: 01142.0122 SEQUENCE LISTING
; CURRENT APPLICATION NUMBER: US/08/816,011F
; CURRENT FILING DATE: 1997-03-11
; PRIOR APPLICATION NUMBER: 08/332,312
; PRIOR FILING DATE: 1994-10-31
; PRIOR APPLICATION NUMBER: PCT/US95/14364
; PRIOR FILING DATE: 1995-10-25
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 18
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-08-816-011F-18
```

Query Match 2.1%; Score 6; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 215 VCSVWG 220
|||||
DB 8 VCSVWG 13

RESULT 7
PCT-US01-28124A-17
; Sequence 17, Application PC/TUS0128124A
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Biopanning and Rapid Analysis of Selective Interactive Ligands (H
; FILE REFERENCE: 005774.P004PCT
; CURRENT APPLICATION NUMBER: PCT/US01/28124A
; CURRENT FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 289
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(7)
; OTHER INFORMATION: synthetic construct
PCT-US01-28124A-17

Query Match 1.8%; Score 5; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 206 LSGSL 210
|||||
DB 3 LSGSL 7

RESULT 8
US-09-881-636-38
; Sequence 38, Application US/09881636
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Arthur B. Raitano
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 55P4H: GENE EXPRESSED IN VARIOUS
; FILE REFERENCE: 129.12USU1
; CURRENT APPLICATION NUMBER: US/09/881,636
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: 60/211,454
; PRIOR FILING DATE: 2000-06-13
; NUMBER OF SEQ ID NOS: 720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-881-636-38

Query Match 1.8%; Score 5; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 DVLRL 23
|||||

DB 3 DVLRL 7
|||||

RESULT 9
US-09-881-636-61
; Sequence 61, Application US/09881636
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Arthur B. Raitano
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 55P4H: GENE EXPRESSED IN VARIOUS
; FILE REFERENCE: 129.12USU1
; CURRENT APPLICATION NUMBER: US/09/881,636
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: 60/211,454
; PRIOR FILING DATE: 2000-06-13
; NUMBER OF SEQ ID NOS: 720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-881-636-61

Query Match 1.8%; Score 5; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 DVLRL 23
|||||
DB 5 DVLRL 9

RESULT 10
US-09-881-636-128
; Sequence 128, Application US/09881636
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Arthur B. Raitano
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 55P4H: GENE EXPRESSED IN VARIOUS
; FILE REFERENCE: 129.12USU1
; CURRENT APPLICATION NUMBER: US/09/881,636
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: 60/211,454
; PRIOR FILING DATE: 2000-06-13
; NUMBER OF SEQ ID NOS: 720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 128
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-881-636-128

Query Match 1.8%; Score 5; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 DVLRL 23
|||||

Db 5 DVLRL 9

RESULT 11

```
US-09-881-636-236
; Sequence 236, Application US/09881636
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Arthur B. Raitano
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 55P4H4: GENE EXPRESSED IN VARIOUS
; FILE REFERENCE: 129.12USU1
; CURRENT APPLICATION NUMBER: US/09/881,636
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: 60/211,454
; PRIOR FILING DATE: 2000-06-13
; NUMBER OF SEQ ID NOS: 720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 236
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-881-636-236
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Query Match 1.8%; Score 5; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 DVLRL 23

Db 5 DVLRL 9

RESULT 12

```
US-09-881-636-339
; Sequence 339, Application US/09881636
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Arthur B. Raitano
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 55P4H4: GENE EXPRESSED IN VARIOUS
; FILE REFERENCE: 129.12USU1
; CURRENT APPLICATION NUMBER: US/09/881,636
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: 60/211,454
; PRIOR FILING DATE: 2000-06-13
; NUMBER OF SEQ ID NOS: 720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 339
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-881-636-339
```

Query Match 1.8%; Score 5; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 DVLRL 23

Db 5 DVLRL 9

RESULT 13

```
US-09-881-636-426
; Sequence 426, Application US/09881636
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Arthur B. Raitano
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 55P4H4: GENE EXPRESSED IN VARIOUS
; FILE REFERENCE: 129.12USU1
; CURRENT APPLICATION NUMBER: US/09/881,636
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: 60/211,454
; PRIOR FILING DATE: 2000-06-13
; NUMBER OF SEQ ID NOS: 720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 426
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-881-636-426
```

Query Match 1.8%; Score 5; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 DVLRL 23

Db 5 DVLRL 9

RESULT 14

```
US-09-881-636-532
; Sequence 532, Application US/09881636
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Arthur B. Raitano
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 55P4H4: GENE EXPRESSED IN VARIOUS
; FILE REFERENCE: 129.12USU1
; CURRENT APPLICATION NUMBER: US/09/881,636
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: 60/211,454
; PRIOR FILING DATE: 2000-06-13
; NUMBER OF SEQ ID NOS: 720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 532
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-881-636-532
```

Query Match 1.8%; Score 5; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 DVLRL 23

Db 5 DVLRL 9

RESULT 15
US-09-881-636-633
; Sequence 633, Application US/09881636
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Rene S. Hubert
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Elana Levin
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Arthur B. Raitano
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: 55P4H4: GENE EXPRESSED IN VARIOUS
; FILE REFERENCE: 129,12USU1
; CURRENT APPLICATION NUMBER: US/09/881,636
; PRIOR FILING DATE: 2001-06-13
; PRIOR FILING DATE: 2000-06-13
; NUMBER OF SEQ ID NOS: 720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 633
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-881-636-633

Query Match 1.8%; Score 5; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 19 DVTRL 23
Db 5 DVTRL 9

Search completed: January 24, 2002, 16:28:29
Job time: 189 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 24, 2002, 16:24:35 ; Search time 16.34 Seconds

(without alignments)
1319.302 Million cell updates/sec

Title: US-08-741-095b-26

Perfect score: 283
Sequence: 1 MEPPDWMGPPMRSPRPTDV.....VITVAVEETIPSTGRSPNH 283

Scoring table: OLIGO
Gapop 60.0 , Gapept 60.0

Searched: 219241 seqs, 76174552 residues

Word size: 0

Total number of hits satisfying chosen parameters: 6208

Minimum DB seq length: 0
Maximum DB seq length: 30

Post-processing: Listing first 45 summaries

Database: PIR.68:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5	1.8	6	2	PT0715
2	5	1.8	10	2	B43590
3	5	1.8	10	2	A43590
4	5	1.8	10	2	PA0050
5	5	1.8	13	2	PC4055
6	5	1.8	15	2	S14749
7	5	1.8	16	2	PH0773
8	5	1.8	17	2	A47678
9	5	1.8	18	2	S58277
10	5	1.8	20	2	P00688
11	5	1.8	20	2	P00687
12	5	1.8	21	2	I40157
13	5	1.8	21	2	I58423
14	5	1.8	24	2	T42257
15	5	1.8	26	1	MEHBCD
16	5	1.8	26	1	S38295
17	5	1.8	26	2	A57221
18	5	1.8	26	2	B84724
19	5	1.8	26	2	A39466
20	5	1.8	30	2	S15678
21	5	1.4	5	2	C23751
22	4	1.4	5	2	PT0714
23	4	1.4	5	2	G44817
24	4	1.4	5	2	I44817
25	4	1.4	5	2	E44817
26	4	1.4	5	2	C44817
27	4	1.4	5	2	A44817
28	4	1.4	5	2	H44817
29	4	1.4	5	2	F44817

30	4	1.4	5	2	B44817	34.5K structural p
31	4	1.4	5	2	D44817	35K structural pro
32	4	1.4	6	2	PT0629	T-cell receptor be
33	4	1.4	6	2	PT0512	T-cell receptor be
34	4	1.4	7	2	PT0728	T-cell receptor be
35	4	1.4	8	2	S08995	hyperrenaloemic
36	4	1.4	8	2	A49823	adipokineic hormo
37	4	1.4	8	2	A44960	neuropeptide Iad-C
38	4	1.4	8	2	A43976	hyperrenaloemic
39	4	1.4	8	2	B43976	hyperrenaloemic
40	4	1.4	8	2	S11545	adipokineic hormo
41	4	1.4	8	2	A05169	neuropeptide M-1 -
42	4	1.4	9	2	A91466	oxytocin - hippo
43	4	1.4	9	2	A92774	oxytocin - spotted
44	4	1.4	9	2	A93147	oxytocin - flinback
45	4	1.4	9	2	A93408	oxytocin - Austral

ALIGNMENTS

RESULT 1
PT0715
T-cell receptor beta chain V-D-J region (165-3A) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0715
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A:Reference number: PT0509; MUID:91277601
A:Accession: PT0715
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-6 <PEE>
C:Keywords: T-cell receptor
C:Experimental source: newborn thymus, strain BALB/c

Query Match 1.8%; Score 5; DB 2; Length 6;
Best local similarity 100.0%; Pred. No. 2.2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 144 SSPQ 148
DB 2 SSPQ 6

RESULT 2
B43590
p1lin type Ae6 - Aeromonas hydrophila (fragment)
C:Species: Aeromonas hydrophila
C>Date: 12-Jan-1993 #sequence_revision 12-Jan-1993 #text_change 17-Nov-2000
C:Accession: B43590
R:Hokama, A.; Iwanaga, M.
Infect. Immun. 59, 3478-3483, 1991
A:Title: Purification and characterization of Aeromonas sobria p1lin, a possible colon
A:Reference number: A43590; MUID:91372953
A:Accession: B43590
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <HOK>
C:Superfamily: Vibrio cholerae prepilin-like 17.3K protein type 4

Query Match 1.8%; Score 5; DB 2; Length 10;
Best local similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 210 LVIV 214
DB 6 LVIV 10

```
RESULT 3
A:Accession: A43590
C:Species: Aeromonas sobria (fragment)
C:Date: 12-Jan-1993 #sequence_revision 12-Jan-1993 #text_change 18-Jun-1993
R:Hokama, A.; Iwanaga, M.
Infect. Immun. 59, 3478-3483, 1991
A:Title: Purification and characterization of Aeromonas sobria pili, a possible coloniza
A:Reference number: A43590; MUID:91372953
A:Accession: A43590
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <HOK>

Query Match
Best Local Similarity 100.0%; Score 5; DB 2; Length 10;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 210 LVIVI 214
DB 6 LVIVI 10

RESULT 4
PA0050
protein QA10052 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C:Accession: PA0050; PA0107
R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A:Description: Separation and characterization of Arabidopsis proteins by two-dimensiona
A:Reference number: PA0001
A:Accession: PA0050
A:Molecule type: protein
A:Residues: 1-10 <KAM>
R:Kamo, M.; Kawakami, T.; Tsugita, A.
submitted to JIPID, March 1995
A:Reference number: PA0109
A:Accession: PA0107
A:Molecule type: protein
A:Residues: 1-10 <KAM>
A:Experimental source: root

Query Match
Best Local Similarity 100.0%; Score 5; DB 2; Length 10;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 142 ATSSP 146
DB 1 ATSSP 5

RESULT 5
PC4055
hypothetical 13 protein - Frankia sp. (fragment)
C:Species: Frankia sp.
C:Date: 10-Sep-1995 #sequence_revision 27-Oct-1995 #text_change 27-Oct-1995
C:Accession: PC4055
R:Harriott, O.T.; Hosted, T.J.; Benson, D.R.
Gene 161, 63-67, 1995
A:Title: Sequences of nifX, nifM, nifZ, nifB and two ORF in the Frankia nitrogen fixatio
A:Reference number: Jc4203; MUID:95369734
A:Accession: PC4055
A:Molecule type: DNA
A:Residues: 1-13 <HAR>
A:Cross-references: GB:L29299
```

```
Query Match
Best Local Similarity 100.0%; Score 5; DB 2; Length 13;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 252 ATYIE 256
DB 5 ATYIE 9

RESULT 6
S14749
3-dehydroquinase - Neurospora crassa (fragment)
C:Species: Neurospora crassa
C:Date: 21-Nov-1993 #sequence_revision 01-Sep-1995 #text_change 01-Sep-1995
C:Accession: S14749
R:Chaudhuri, S.; Duncan, K.; Graham, L.D.; Cogging, J.R.
Biochem. J. 275, 1-6, 1991
A:Title: Identification of the active-site lysine residues of two biosynthetic 3-dehy
A:Reference number: S14749; MUID:91207275
A:Accession: S14749
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <CHA>
```

```
Query Match
Best Local Similarity 100.0%; Score 5; DB 2; Length 15;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 232 GDVVK 236
DB 5 GDVVK 9
```

```
RESULT 7
PH0773
T-cell receptor beta chain (C7) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C:Accession: PH0773
R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility comple
allelic exclusion and antigen-specific repertoire.
A:Reference number: PH0746; MUID:92078846
A:Accession: PH0773
A:Molecule type: mRNA
A:Residues: 1-16 <CAS>
A:Cross-references: EMBL:X60868; NID:950247; PIDN:CAA43257.1; PID:950248
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor
```

```
Query Match
Best Local Similarity 100.0%; Score 5; DB 2; Length 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 144 SSPGQ 148
DB 3 SSPGQ 7
```

```
RESULT 8
AA7678
pilin - Aeromonas sobria (fragment)
C:Species: Aeromonas sobria
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
C:Accession: AA7678
R:Iwanaga, M.; Hokama, A.
J. Gen. Microbiol. 138, 1913-1919, 1992
A:Title: Characterization of Aeromonas sobria TAP13 pili: a possible new colonization
A:Reference number: AA7678; MUID:93018994
A:Contents: TAP13
```

A:Accession: A47678
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-17 <IKWA>
 A:Note: sequence extracted from NCBI backbone (NCBI:116639)
 C:Superfamily: Vbdrlo cholerae prepilin-like 17.3k protein type 4

Query Match 1.8%; Score 5; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 210 LVIV 214
 |||||
 Db 6 LVIV 10

RESULT 9
 S58277
 Insulin-like growth factor receptor type II - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 05-Nov-1999
 C:Accession: S58277
 R:Smrzka, O.W.; Stoger, R.; Kurzbauer, R.; Fae, I.; Fischer, G.F.; Barlow, D.P.
 submitted to the EMBL Data Library, January 1995
 A:Description: Conservation of a methylation imprint and a putative imprinting box at th
 A:Reference number: S58277
 A:Accession: S58277
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-18 <SMR>
 A:Cross-references: EMBL:X83702; NID:9929644; PIDN:CA58675.1; PID:9929645
 C:Keywords: growth factor receptor

Query Match 1.8%; Score 5; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 38 ALPSC 42
 |||||
 Db 10 ALPSC 14

RESULT 10
 PQ0688
 Photosystem I 14.0K E4 chain - common tobacco (fragment)
 C:Species: Nicotiana tabacum (common tobacco)
 C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 17-Mar-1999
 C:Accession: PQ0688
 R:Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugitara, M.
 Plant Physiol. 102, 1259-1267, 1993
 A:Title: Molecular heterogeneity of photosystem I. psad, psaf, psah and psal are
 A:Reference number: PQ0667; MUID:94105345
 A:Accession: PQ0688
 A:Molecule type: protein
 A:Residues: 1-20 <OBO>
 C:Keywords: chloroplast; photosynthesis; photosystem I

Query Match 1.8%; Score 5; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 248 AEGEA 252
 |||||
 Db 13 AEGEA 17

RESULT 11
 PQ0687
 Photosystem I 14.1K E3 chain - common tobacco (fragment)
 C:Species: Nicotiana tabacum (common tobacco)

C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 17-Mar-1999
 C:Accession: PQ0687; PQ0675
 R:Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugitara, M.
 Plant Physiol. 102, 1259-1267, 1993
 A:Title: Molecular heterogeneity of photosystem I. psad, psaf, psah and psal ar
 A:Reference number: PQ0667; MUID:94105345
 A:Accession: PQ0687
 A:Molecule type: protein
 A:Residues: 1-20 <OBO>
 A:Note: this peptide was designated photosystem I 14.1K E3 chain
 A:Accession: PQ0675
 A:Molecule type: protein
 A:Residues: 2-11 <OB2>
 A:Note: this peptide was designated photosystem I 14.0K E4 chain
 C:Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 1.8%; Score 5; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 248 AEGEA 252
 |||||
 Db 14 AEGEA 18

RESULT 12
 I40157
 tetracycline resistance (tet) protein - plasmid pBC16 (fragment)
 C:Species: plasmid pBC16
 C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 26-Aug-1999
 C:Accession: I40157
 R:Metzger, A.
 Appl. Environ. Microbiol. 56, 1128-1134, 1990
 A:Title: Expression of Bacillus thuringiensis delta-endotoxin genes during vegetative
 A:Reference number: I40157; MUID:90253151
 A:Accession: I40157
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-21 <RES>
 A:Cross-references: GB:M34478; NID:g143851; PIDN:AAA98049.1; PID:g143852
 C:Superfamily: tetracycline resistance protein
 C:Keywords: antibiotic resistance; transmembrane protein

Query Match 1.8%; Score 5; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 186 SWLYT 190
 |||||
 Db 6 SWLYT 10

RESULT 13
 I58423
 arylhydrocarbon receptor - mouse
 C:Species: Mus sp. (mouse)
 C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
 C:Accession: I58423
 R:Mimura, J.; Ema, M.; Sogawa, K.; Ikawa, S.; Fujii-Kuriyama, Y.
 Pharmacogenetics 4, 349-354, 1994
 A:Title: A complete structure of the mouse Ah receptor gene.
 A:Reference number: I58423; MUID:95218835
 A:Accession: I58423
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-21 <RES>
 A:Cross-references: GB:S76044; NID:9913085; PIDN:AAB3978.1; PID:9913086
 C:Genetics:
 A:Gene: Ah

Query Match 1.8%; Score 5; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 226 KRRKP 230
 |||||
 Db 13 KRRKP 17

RESULT 14

T42257
 phosphoprotein phosphatase (EC 3.1.3.16) - Caenorhabditis elegans (fragment)
 C:Species: Caenorhabditis elegans
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Jun-2000
 C:Accession: T42257
 R:Zeke, T.; Gergely, P.; Dombradi, V.
 submitted to the EMBL Data Library, July 1996
 A:Description: The catalytic subunits of Ser/Thr protein phosphatases from Caenorhabditis
 A:Reference number: 222131
 A:Accession: T42257
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-24 <2EK>
 A:Cross-references: EMBL:277735; PIDN:CAB01294.1
 C:Superfamily: phosphoprotein phosphatase; phosphoesterase core homology; phosphoprotein
 C:Keywords: phosphoric monoester hydrolase

Query Match 1.8%; Score 5; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 4.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 DVLR 23
 |||||
 Db 4 DVLR 8

RESULT 15

MEHBCD
 mellitin - giant honeybee (tentative sequence)
 C:Species: Apis mellifera dorsata (giant honeybee)
 C:Date: 22-Jun-1981 #sequence_revision 22-Jun-1981 #text_change 31-Mar-2000
 C:Accession: A01763
 R:Krell, G.
 FEBS Lett. 54, 100-102, 1975
 A:Title: The structure of Apis dorsata mellitin: phylogenetic relationships between hone
 A:Reference number: A01763; MUID:75168194
 A:Accession: A01763
 A:Molecule type: protein
 A:Residues: 1-26 <KRE>
 C:Superfamily: mellitin major
 C:Keywords: amidated carboxyl end; homotetramer
 F:26/Modified site: amidated carboxyl end (Glu) #status experimental

Query Match 1.8%; Score 5; DB 1; Length 26;
 Best Local Similarity 100.0%; Pred. No. 5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 243 KRRKP 247
 |||||
 Db 22 KRRKP 26

Search completed: January 24, 2002, 16:26:28
 Job time: 113 sec

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OM protein - protein search, using sw model

Run on: January 24, 2002, 16:26:05 ; Search time 9.83 Seconds

(without alignments)
1055.559 Million cell updates/sec

Title: US-08-741-095b-26

Perfect score: 283

Sequence: 1 MEPPGDMGPPWRSTPRTDV.....VTVVAVETIPSTGSPNH 283

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 100059 seqs, 36664827 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1802

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	1.8	19	1	DHAB_COMTE
2	5	1.8	26	1	LCIP_HUMAN
3	5	1.8	26	1	MELAPIDO
4	4	1.4	4	1	EOSI_HUMAN
5	4	1.4	8	1	CPDI_ENTRA
6	4	1.4	8	1	HTEF_PPRAM
7	4	1.4	8	1	HTEF_TENMO
8	4	1.4	9	1	OXYT_CYPCA
9	4	1.4	9	1	OXYT_RABIT
10	4	1.4	9	1	OXYV_SOUNC
11	4	1.4	10	1	COXH_ONCMY
12	4	1.4	10	1	ESL_LACCA
13	4	1.4	10	1	GS09_BACSU
14	4	1.4	10	1	TRP5_LEUMA
15	4	1.4	11	1	LPW_THERH
16	4	1.4	13	1	TEMC_RANFE
17	4	1.4	13	1	UP71_LITRW
18	4	1.4	14	1	CALI_CALGI
19	4	1.4	14	1	GLPK_STRGR
20	4	1.4	14	1	PSAG_CUCSA
21	4	1.4	14	1	TAT_HVIM2
22	4	1.4	14	1	TAT_HVIM2
23	4	1.4	15	1	DCMW_PSECH
24	4	1.4	15	1	TERM_BPM2
25	4	1.4	15	1	UC19_MAIZE
26	4	1.4	16	1	HRD_CLOPA
27	4	1.4	17	1	YPRK_SALTY
28	4	1.4	20	1	CHP_THICQ
29	4	1.4	20	1	COG2_CHIOP
30	4	1.4	20	1	COG3_CHIOP
31	4	1.4	20	1	COGA_PARCM
32	4	1.4	20	1	COGB_PARCM
33	4	1.4	20	1	COGB_PARCM

34	4	1.4	20	1	RIPX_CUCPE
35	4	1.4	20	1	SODE_PASPI
36	4	1.4	21	1	SCIB_BPT5
37	4	1.4	24	1	CT31_LITCI
38	4	1.4	25	1	ACP_ERYLO
39	4	1.4	25	1	CR21_LITSP
40	4	1.4	25	1	CR22_LITCI
41	4	1.4	25	1	CR23_LITCE
42	4	1.4	25	1	CR24_LITCE
43	4	1.4	25	1	CR25_LITCI
44	4	1.4	25	1	H2B1_ECHES
45	4	1.4	25	1	MT_AGABI

ALIGNMENTS

RESULT	ID	DHAB_COMTE	STANDARD	PRT	19 AA
AC	P80704:				
DT	01-OCT-1996	(Rel. 34, Created)			
DT	01-OCT-1996	(Rel. 34, Last sequence update)			
DT	15-DEC-1998	(Rel. 37, Last annotation update)			
DE	ALDEHYDE DEHYDROGENASE, BETA CHAIN (EC 1.2.99.3) (ALDH) (FRAGMENT).				
OS	Comamonas testosteroni (Pseudomonas testosteroni).				
OC	Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Comamonas.				
OX	NCBI_TaxID=285;				
RM	[1]				
RP	SEQUENCE.				
RC	STRAIN-ATCC 15667;				
RA	Luykx D.M.A.M., Kim S.W., de Vries S., Duine J.A.;				
RL	Submitted (JUL-1996) to the SWISS-PROT data bank.				
CC	-I- CATALYTIC ACTIVITY: AN ALDEHYDE + ACCEPTOR + H(2)O = AN ACID +				
CC	REDUCED ACCEPTOR.				
CC	-I- COFACTOR: MOLYBDENUM.				
CC	-I- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA AND A GAMMA				
CC	CHAIN.				
KM	Oxidoreductase; Molybdenum.				
FT	NON_TER	19			
SQ	SEQUENCE	19 AA: 2096 MW: 89BD67DAD05A212E CRC64;			
Query Match					
Best Local Similarity 1.8%; Score 5; DB 1; Length 19;					
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
OY	14	SNPT 18			
DB	7	STPT 11			
RESULT 2					
ID	LCIP_HUMAN	STANDARD	PRT	26 AA	
AC	P34168:				
DT	01-FEB-1994	(Rel. 28, Created)			
DT	01-FEB-1994	(Rel. 28, Last sequence update)			
DT	20-AUG-2001	(Rel. 40, Last annotation update)			
DE	CHYMOTRYPSIN-LIKE SERINE PROTEINASE (EC 3.4.21.-) (LCIP) (FRAGMENT).				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RM	[1]				
RP	SEQUENCE.				
RC	TISSUE=Lung;				
RX	MEDLINE=94092341; PubMed=8267879;				
RA	Heidmann H.-H., Travis J.;				
RT	"A novel chymotrypsin-like serine proteinase from human lung.;"				
RL	Biol. Chem. Hoppe-Seyler 374:871-875(1993).				
CC	-I- FUNCTION: SPECIFICITY SIMILAR TO CHYMOTRYPSIN.				
CC	-I- ENZYME REGULATION: INHIBITED BY DFP, TOSYL-PHENYLANILYL-				

CC CHLOROMETHANE, CHYMOTRISTIN, SOYBEAN TRYPSIN INHIBITOR,
 CC ALPHA-1-ANTI-CHYMOTRYPSIN AND ALPHA-2-MACROGLOBULIN.
 CC -1- PTM: EXTENSIVELY GLYCOSYLATED.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY.
 DR PIR: S38295; S38295.
 DR HSSP: P23946; 1KLT.
 DR MEROPS: S01.311; .
 DR InterPro: IPR001254; Trypsin.
 DR Pfam: PF00089; trypsin; 1.
 DR PROSITE: PS50240; TRYPSIN_DOM; PARTIAL.
 DR PROSITE: PS00134; TRYPSIN_HIS; PARTIAL.
 DR PROSITE: PS00135; TRYPSIN_SER; PARTIAL.
 KW Hydrolase; Serine protease; Glycoprotein.
 FT NON_TER
 SQ SEQUENCE 26 AA: 2822 MW: 83747d477AAC52F5 CRC64;

Query Match 1.8%; Score 5; DB 1; Length 26;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 153 GGTS 157
 DB 3 GGTS 7

RESULT 3
 ID MEL_APIDO STANDARD; PRT; 26 AA.
 AC P01502;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE MELITTIN.
 OS Apis dorsata (Giant honeybee).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Apidae; Apis.
 OX NCBI_TaxID=7462;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=75168194; PubMed=1093875;
 RA Krell G.;
 RT "The structure of Apis dorsata mellitin: phylogenetic relationships
 RT between honeybees as deduced from sequence data.";
 RL FEBS Lett. 54:100-102(1975).
 CC -1- FUNCTION: MAIN TOXIN OF BEE VENOM WITH STRONG HEMOLYTIC ACTIVITY.
 CC INTEGRATES INTO CELL MEMBRANES AND HAS MULTIPLE EFFECTS, PROBABLY,
 CC AS A RESULT OF ITS INTERACTION WITH NEGATIVELY CHARGED
 CC PHOSPHOLIPIDS. IT INHIBITS WELL KNOWN TRANSPORT PUMPS SUCH AS THE
 CC NA(+)-K(+)-ATPASE AND THE H(+)-K(+)-ATPASE. INCREASES THE
 CC PERMEABILITY OF CELL MEMBRANES TO IONS, PARTICULARLY NA+ AND
 CC INDIRECTLY CA2+, BECAUSE OF THE NA(+)-CA(2+)-EXCHANGE.
 CC -1- SUBUNIT: MONOMER AND HOMOTETRAMER (BY SIMILARITY).
 CC -1- DATABASE: NAME-Protein Spotlight;
 CC NOTE-Issue 12 of July 2001;
 CC WWW="http://www.expasy.org/spotlight/articles/spotlit012.html".
 DR PIR: A01763; MEHBCD.
 DR HSSP: P01501; 2MLT.
 DR InterPro: IPR002116; Melittin.
 DR Pfam: PF01372; Melittin; 1.
 DR ProDom: PD014636; Melittin; 1.
 KW Hemolysis; Toxin; Venom; Amidation.
 FT MOD_RES 26
 SQ SEQUENCE 26 AA: 2848 MW: F1DA6F92514EF01C CRC64;

Query Match 1.8%; Score 5; DB 1; Length 26;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 243 RRROE 247

DB 22 RRROE 26

RESULT 4
 ID EOSI_HUMAN STANDARD; PRT; 4 AA.
 AC P02731;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1986 (Rel. 01, Last annotation update)
 DE EOSINOPHILOTACTIC PEPTIDES.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=76078412; PubMed=1060093;
 RA Goetzl E.J.; Austen K.F.;
 RT "Purification and synthesis of eosinophilotactic tetrapeptides of
 RT human lung tissue: Identification as eosinophil chemotactic factor of
 RT anaphylaxis.";
 RL Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).
 CC -1- MISCELLANEOUS: THESE PEPTIDES ARE RELEASED FROM MAST CELLS IN LUNG
 CC (AND OTHER TISSUES) DURING HYPERSENSITIVITY REACTIONS
 CC (ANAPHYLAXIS). THEIR ACTIVITIES, PREFERENTIALLY AFFECTING
 CC EOSINOPHILS, INCLUDE CHEMOTAXIS, CHEMOTACTIC DEACTIVATION, RELEASE
 CC OF ENZYMES, AND STIMULATION OF THE HEXOSE MONOPHOSPHATE SHUNT.
 DR PIR: A03190; ETHDL.
 DR VARIANT 1 V -> A (IN OTHER PEPTIDE).
 FT FT
 SQ SEQUENCE 4 AA: 390 MW: 6B05B862A0000000 CRC64;

Query Match 1.4%; Score 4; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 49 VGSE 52
 DB 1 VGSE 4

RESULT 5
 ID CPD1_ENTFA STANDARD; PRT; 8 AA.
 AC P13269;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE SEX PHEROMONE CPD1.
 OS Enterococcus faecalis (Streptococcus faecalis).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
 OC Enterococcus.
 OX NCBI_TaxID=1351;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=85040388; PubMed=6436978;
 RA Suzuki A., Mori M., Sagakami Y., Isogai A., Fujino M., Kitada C.,
 RA Craig R.A., Clevel D.B.;
 RT "Isolation and structure of bacterial sex pheromone, CPD1.";
 RL Science 226:849-850(1984).
 CC -1- FUNCTION: CPD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
 CC BACTERIOCIN PLASMID PPDI.
 KW Pheromone.
 SQ SEQUENCE 8 AA: 913 MW: 8665B729C682C729 CRC64;

Query Match 1.4%; Score 4; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 205 FLSG 208
 ||||
 Db 5 FLSG 8

RESULT 6

HTFL_PERAM STANDARD: PRT: 8 AA.
 AC P04548;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE HYPERTREHALOASEMIC FACTOR I (NEUROPEPTIDE M-1) (PERIPLANETIN CC-1)
 DE (PEA-CAH-1) (LED-CC-1) (HYPERTREHALOASEMIC NEUROPEPTIDE I).
 OS Periplaneta americana (American cockroach),
 OS Leptinotarsa decemlineata (Colorado potato beetle), and
 OS Blatta orientalis (Oriental cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blattodea; Blattidae; Periplaneta.
 OX NCBI_TaxID=6978, 7539, 6976;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=P.americana;
 RX MEDLINE=85046530; PubMed=6548628;
 RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
 RA Rinehart K.L. Jr.;
 RT *Structures of two cockroach neuropeptides assigned by fast atom
 RT bombardment mass spectrometry.";
 RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=P.americana;
 RX MEDLINE=84298179; PubMed=6591205;
 RA Scarbrough R.M., Jamison G.C., Kalish F., Kramer S.J., McEnroe G.A.,
 RA Miller C.A., Schooley D.A.;
 RT *Isolation and primary structure of two peptides with
 RT cardioacceleratory and hyperglycemic activity from the corpora
 RT cardiaca of Periplaneta americana.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
 RX MEDLINE=90160053; PubMed=2576128;
 RA Gaede G., Kellner R.;
 RT "The metabolic neuropeptides of the corpus cardiaca from the potato
 RT beetle and the American cockroach are identical.";
 RL Peptides 10:1287-1289(1989).
 RN [4]
 RP SEQUENCE.
 RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
 RX MEDLINE=90253659; PubMed=2340112;
 RA Gaede G., Rinehart K.L. Jr.;
 RT "Primary structures of hypertrehalosemic neuropeptides isolated from
 RT the corpora cardiaca of the cockroaches Leucophaea maderae,
 RT Gromphodoria portoricensis, Blattella germanica and Blatta orientalis
 RT and of the stick insect Extatosoma tiaratum assigned by tandem fast
 RT atom bombardment mass spectrometry.";
 RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
 CC -1- FUNCTION: HYPERTREHALOASEMIC FACTORS ARE NEUROPEPTIDES THAT
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
 CC -1- SIMILARITY: BELONGS TO THE AKH / HRTM / RPCH FAMILY.
 CC PIR: A05169; A05169.
 DR PIR: S08995; S08995.
 DR PIR: A49823; A49823.
 DR PIR: A44960; A44960.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 KM Neuropeptide; Amidation.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 FT SEQUENCE 8 AA; 991 MW; 86745775B9C452D6 CRC64;

Query Match 1.4%; Score 4; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 170 FSPN 173
 ||||
 Db 4 FSPN 7

RESULT 7

HTE_TENMO STANDARD: PRT: 8 AA.
 AC P25419;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE HYPERTREHALOASEMIC FACTOR (HOTH) (HYPERTREHALOASEMIC NEUROPEPTIDE).
 OS Tenebrio molitor (Yellow mealworm), and Zophobas rugipes.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
 OC Cucujiformia; Tenebrionidae; Tenebrio.
 OX NCBI_TaxID=7067, 7075;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=90341081; PubMed=2381871;
 RA Gaede G., Rosinski G.;
 RT "The primary structure of the hypertrehalosemic neuropeptide from
 RT tenebrionid beetles: a novel member of the AKH/RPCH family.";
 RL Peptides 11:455-459(1990).
 CC -1- FUNCTION: HYPERTREHALOASEMIC FACTORS ARE NEUROPEPTIDES THAT
 CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
 CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
 CC -1- SIMILARITY: BELONGS TO THE AKH / HRTM / RPCH FAMILY.
 CC PIR: A43976; A43976.
 DR PIR: B43976; B43976.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 KM Neuropeptide; Amidation.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 FT SEQUENCE 8 AA; 1005 MW; 86745775B9C44736 CRC64;

Query Match 1.4%; Score 4; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 170 FSPN 173
 ||||
 Db 4 FSPN 7

RESULT 8
 OXYT_CYPCA STANDARD: PRT: 9 AA.
 AC P23879;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE VASOTOCIN.
 OS Cyprinus carpio (Common carp), and Petromyzon marinus (Sea lamprey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
 OX NCBI_TaxID=7962, 7757;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=C.carpio; TISSUE=Plutitary;
 RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
 RT "Characterization of neurohypophyseal hormones from a fresh water bony

RT fish, the carp (*Cyprinus carpio*). Comparison with hormones from sea
 RT water bony fish.":
 RT Comp. Biochem. Physiol. 14:245-254(1965).
 RN [2]
 RP SEQUENCE.
 RC SPECIES-P.marinus; TISSUE-Pituitary;
 RX MEDLINE=88225976; PubMed=3371648;
 RA Lane T.F., Sower S.A., Kawachi H.;
 RT "Arginine vasotocin from the pituitary gland of the lamprey
 (Petromyzon marinus): Isolation and amino acid sequence.";
 RL Gen. Comp. Endocrinol. 70:152-157(1988).
 CC -1- FUNCTION: ANTIDIURETIC HORMONE.
 CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
 DR PIR: B61364; B61364.
 DR PIR: S06375; S06375.
 DR InterPro: IPR000981; Neurohypophys_horm.
 DR Pfam: PF00220; hormone4; 1.
 DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
 DR Hormone; Amidation.
 FT DISULFID 1 6
 FT MOD.RES 9 9 AMIDATION
 SQ SEQUENCE 9 AA: 1053 MW; 17EB176EB456D04B CRC64;

Query Match 1.4%; Score 4; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No.1e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 163 ONCP 166
 DB 4 ONCP 7

RESULT 9
 OXYT_RABIT STANDARD: PRT: 9 AA.
 ID OXYT_RABIT
 AC P32878; P01188;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE OXYTOCIN (OXYTOCIN).
 OS Oryctolagus cuniculus (Rabbit). Hippopotamus amphibius (Hippopotamus),
 OS Balenoptera physalus (Finback whale) (Common rorqual), and
 OS Tachyglossus aculeatus aculeatus (Australian echidna), and
 OS Hydroloagus collei (Spotted ratfish) (Pacific ratfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 NCBI_TaxID=9986, 9833, 9770, 49271, 7873;
 RN [1]
 RP SEQUENCE.
 RC SPECIES-Rabbit;
 RX MEDLINE=72215060; PubMed=5150741;
 RA Chauvet J., Chauvet M.-T., Acher R.;
 RT "Evolution of neurohypophyseal hormones: Isolation of active
 RT principles from rabbits and rats.";
 RL Biochimie 53:1099-1104(1971).
 RN [2]
 RP SEQUENCE.
 RC SPECIES-H.amphibius;
 RX MEDLINE=71232719; PubMed=5406007;
 RA Ferguson D.R., Pickering B.T.;
 RT "Arginine and lysine vasopressins in the hippopotamus
 RT neurohypophysis.";
 RL Gen. Comp. Endocrinol. 13:425-429(1969).
 RN [3]
 RP SEQUENCE.
 RC SPECIES-B.physalus;
 RA Acher R., Chauvet J., Chauvet M.-T.;
 RT "Isolation of finback whale oxytocin and vasopressin.";
 RL Nature 201:191-192(1964).
 RN [4]
 RP SEQUENCE.
 RC SPECIES-A.aculeatus;

RX MEDLINE=73223515; PubMed=4515919;
 RA Acher R., Chauvet J., Chauvet M.-T.;
 RT "Neurohypophysial hormones and evolution of tetrapods.";
 RN Nature New Biol. 244:124-126(1973).
 RN [5]
 RP SEQUENCE.
 RC SPECIES-H.collei;
 RX MEDLINE=70088110; PubMed=5366118;
 RA Pickering B.T., Heller H.;
 RT "Oxytocin as a neurohypophysial hormone in the holoccephalian
 RT elasmobranch fish, *Hydroloagus collei*.";
 RL J. Endocrinol. 45:597-606(1969).
 CC -1- FUNCTION: OXYTOCIN CAUSES CONTRACTION OF THE SMOOTH MUSCLE OF THE
 CC UTERUS AND OF THE MAMMARY GLAND.
 CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
 DR PIR: A91466; A91466.
 DR PIR: A92774; A92774.
 DR PIR: A93147; A93147.
 DR PIR: A93408; A93408.
 DR PIR: B90667; B90667.
 DR PDB: 1XY1; 15-OCT-90.
 DR PDB: 1XY2; 15-OCT-90.
 DR InterPro: IPR000981; Neurohypophys_horm.
 DR Pfam: PF00220; hormone4; 1.
 DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
 DR Hormone; Hypothalamus; Amidation; 3D-structure.
 FT DISULFID 1 6
 FT MOD.RES 9 9 AMIDATION
 SQ SEQUENCE 9 AA: 1010 MW; 17F8376EB456D04B CRC64;

Query Match 1.4%; Score 4; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No.1e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 163 ONCP 166
 DB 4 ONCP 7

RESULT 10
 OXYV_SQUAC STANDARD: PRT: 9 AA.
 ID OXYV_SQUAC
 AC P43000;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE VALITOCIN.
 OS Squalus acanthias (Spiny dogfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.
 NCBI_TaxID=7797;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=73031727; PubMed=5083097;
 RA Acher R., Chauvet J., Chauvet M.-T.;
 RT "Phylogeny of the neurohypophysial hormones. Two new active peptides
 RT isolated from a cartilaginous fish, *Squalus acanthias*.";
 RL Eur. J. Biochem. 29:12-19(1972).
 RN [2]
 RP SEQUENCE.
 RX MEDLINE=72128038; PubMed=4622083;
 RA Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
 RT "Identification of 2 new neurohypophyseal hormones, valitocin (Vali-
 RT oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the
 RT spiny dog-fish (*Squalus acanthias*).";
 RL C. R. Acad. Sci., D, Sci. Nat. 274:313-316(1972).
 CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
 DR InterPro: IPR000981; Neurohypophys_horm.
 DR Pfam: PF00220; hormone4; 1.
 DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
 DR Hormone; Amidation.
 FT DISULFID 1 6

FT MOD.RES 9 9 AMINATION.
SQ SEQUENCE 9 AA: 996 MW: 17EDD76EB456D04B CRC64:

Query Match 1.4%; Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 163 QNCP 166
DB 4 QNCP 7

RESULT 11

COXH_ONCMY STANDARD; PRT: 10 AA.
AC P80331;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DE CYTOCHROME C OXIDASE POLYPEPTIDE VIC (EC 1.9.3.1) (FRAGMENT).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxId=8022;
RN [1]
RP SEQUENCE.

RC TISSUE=Liver;
RX MEDLINE=94237150; PubMed=8181469;
RA Freund R., Kadenbach B.;
RT "Identification of tissue-specific isoforms for subunits Vb and VIIa of cytochrome c oxidase isolated from rainbow trout.";
RT Eur. J. Biochem. 221:1111-1116(1994).

CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.

CC -1- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4 FERRICYTOCHROME C.

CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.

DR PIR: S43630; S43630.

KW Oxidoreductase; Inner membrane; Mitochondrion.

FT NON_TER 10 10
SQ SEQUENCE 10 AA: 977 MW: E11B40769DC772DA CRC64:

Query Match 1.4%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 101 PAMG 104
DB 5 PAMG 8

RESULT 12

ESL_LACCA STANDARD; PRT: 10 AA.
AC P81758;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE PUTATIVE ESTERASE/LIPASE (EC 3.1.1.-) (FRAGMENT).

OS Lactobacillus casei.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
OC Lactobacillus.

OX NCBI_TaxId=1582;
RN [1]
RP SEQUENCE.

RC STRAIN=IFPL731.
RA Lopez de Felipe F.;
RT Submitted (MAR-1999) to the SWISS-PROT data bank.
KW Hydrolase; Serine esterase.

FT NON_TER 10 10
SQ SEQUENCE 10 AA: 1070 MW: 1C6132D732CAB1A0 CRC64:

Query Match 1.4%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 TDVL 21
DB 4 TDVL 7

RESULT 13

GS09_BACSU STANDARD; PRT: 10 AA.
AC P80243;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE GENERAL STRESS PROTEIN 9 (GSP9) (FRAGMENT).

GN YZF.

OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.

OX NCBI_TaxId=1423;
RN [1]
RP SEQUENCE.

RC STRAIN=IS58;
RX MEDLINE=94282319; PubMed=8012595;
RA Voelker U., Engelmann S., Maul B., Rietdorf S., Voelker A.,
RA Schmelz R., Mach H., Hecker M.;

RT "Analysis of the induction of general stress proteins of Bacillus subtilis.";
RT Microbiology 140:741-752(1994).

CC -1- INDUCTION: BY HEAT SHOCK, SALT STRESS, OXIDATIVE STRESS, GLUCOSE LIMITATION AND OXYGEN LIMITATION.

DR Subtilisin; BG19022; yzf.

KW Heat shock; Complete proteome.

FT NON_TER 10 10
SQ SEQUENCE 10 AA: 1168 MW: 99764442D5A2C05A CRC64:

Query Match 1.4%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 238 IVSV 241
DB 4 IVSV 7

RESULT 14

TRP5_LEUMA STANDARD; PRT: 10 AA.
AC P81737;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE TACHYKININ-RELATED PEPTIDE 5 (LEMTP 5).

OS Leucophaea maderae (Madeira cockroach).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthoptera; Dictyoptera; Blattaria;

OC Blaberoidae; Blaberidae; Leucophaea.

OX NCBI_TaxId=6988;
RN [1]
RP SEQUENCE.

RC TISSUE=Midgut;
RX MEDLINE=97053012; PubMed=8897641;

RA Muren J.E., Naessel D.R.;
RT "Isolation of five tachykinin-related peptides from the midgut of the cockroach Leucophaea maderae: existence of N-terminally extended isoforms.";

RL Regu1. Pept. 65:185-196(1996).
 RN [2]
 RP SEQUENCE. AND MASS SPECTROMETRY.
 RC TISSUE-Brain; PubMed-9114447;
 RX MEDLINE-97269266; PubMed-9114447;
 RA Muren J.E., Naessel D.R.;
 RT "Seven tachykinin-related peptides isolated from the brain of
 RT madeira cockroach: evidence for tissue-specific expression of
 RT isoforms."
 RT Peptides 18:7-15(1997).
 RL -1- FUNCTION: MYOACTIVE PEPTIDE. INCREASES THE AMPLITUDE AND FREQUENCY
 CC OF SPONTANEOUS CONTRACTIONS AND TONUS OF HINDGUT MUSCLE.
 CC -1- TISSUE SPECIFICITY: MIDGUT AND BRAIN.
 CC -1- MASS SPECTROMETRY: MW-1033.2; METHOD-MALDI.
 CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD.RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1033 MW; C452CD6D9C8769D CRC64;

Query Match 1.4%; Score 4; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred.No.1.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 101 PAMG 104
 Db 2 PAMG 5

RESULT 15
 LPW_THERM STANDARD; PRT; 11 AA.
 ID LPW_THERM
 AC P05624;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE TRP OPERON LEADER PEPTIDE.
 GN TRPL.
 OS Thermus aquaticus (subsp. thermophilus).
 OC Bacteria; Thermus/Delnococcus group; Thermus group; Thermus.
 OX NCBI_TaxID=274;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-HB8 / ATCC 27634;
 RX MEDLINE-89000781; PubMed-2844259;
 RA Sato S., Nakada Y., Kanaya S., Tanaka T.;
 RT "Molecular cloning and nucleotide sequence of Thermus thermophilus
 RT HB8 trpE and trpG."
 RL Biochim. Biophys. Acta 950:303-312(1988).
 CC -1- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
 CC OF TRYPTOPHAN.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X07744; CAA30565.1; -
 DR PIR: S03315; LEFTME.
 KW Tryptophan biosynthesis; Leader peptide.
 SQ SEQUENCE 11 AA; 1228 MW; 364B295A772DC5A7 CRC64;

Query Match 1.4%; Score 4; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred.No.1.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 38 ALPS 41
 Db 2 ALPS 5

Search completed: January 24, 2002, 16:29:16
 Job time: 191 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 24, 2002, 16:25:50 ; Search time 23.62 seconds
(without alignments)
1752.543 Million cell updates/sec

Title: US-08-741-095b-26

Perfect score: 283
Sequence: 1 MEPPGDMGPPMWRSTPRTDV.....VTVVAVETIPSTGRSPNH 283

Scoring table: OLIGO
Gapop 60.0 , Capext 60.0

Searched: 473505 seqs, 146272329 residues

Word size : 0

Total number of hits satisfying chosen parameters: 12410

Minimum DB seq length: 0

Maximum DB seq length: 30

Post-processing: Listing first 45 summaries

Database :

1: SPREMBL_17:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5	1.8	10	09R5T6	09R5T6 aeromonas s
2	5	1.8	14	09FUX5	09FUX5 symphoricar
3	5	1.8	16	09R4T3	09R4T3 mycobacteri
4	5	1.8	17	09R5G4	09R5G4 aeromonas s
5	5	1.8	17	09R5G4	09R5G4 aeromonas s
6	5	1.8	20	09R5B9	09R5B9 spinacia ol
7	5	1.8	20	09R5B9	09R5B9 aeromonas s
8	5	1.8	20	09T2I9	09T2I9 nicotiana s
9	5	1.8	20	09T2I8	09T2I8 nicotiana s
10	5	1.8	21	09T2I8	09T2I8 nicotiana s
11	5	1.8	24	09R4B4	09R4B4 caenorhabdi
12	5	1.8	25	09R4B4	09R4B4 aeromonas t
13	5	1.8	25	09R4B4	09R4B4 homo sapien
14	5	1.8	25	09R4B4	09R4B4 homo sapien
15	5	1.8	25	09R4B4	09R4B4 human immu
16	5	1.8	25	09R4B4	09R4B4 human immu
17	5	1.8	26	09R4B4	09R4B4 arabidopsi
18	5	1.8	28	09R4B4	09R4B4 homo sapien
19	5	1.8	30	09R4B4	09R4B4 homo sapien

20	4	1.4	7	12	09YVE3	09YVE3 human adeno
21	4	1.4	7	12	09YIR0	09YIR0 human adeno
22	4	1.4	7	12	09YIO9	09YIO9 human adeno
23	4	1.4	9	6	09YUVO	09YUVO monodelphis
24	4	1.4	9	6	09YUVO	09YUVO monodelphis
25	4	1.4	10	5	09TLM7	09TLM7 laurancia v
26	4	1.4	10	10	09R2B4	09R2B4 dirosophila
27	4	1.4	10	12	09R2B4	09R2B4 aegilops sq
28	4	1.4	10	12	085598	085598 moloney mur
29	4	1.4	11	4	085619	085619 moloney mur
30	4	1.4	11	4	016217	016217 homo sapien
31	4	1.4	11	8	079921	079921 phynocoepta
32	4	1.4	11	8	079986	079986 laudakia er
33	4	1.4	11	8	079985	079985 laudakia ca
34	4	1.4	11	8	096673	096673 ctenophorus
35	4	1.4	11	8	096649	096649 otocryptis
36	4	1.4	11	8	096637	096637 calotes llo
37	4	1.4	11	8	0965X4	0965X4 tirapelus ag
38	4	1.4	11	8	0965W8	0965W8 tirapelus sa
39	4	1.4	11	8	0965W5	0965W5 laudakia nu
40	4	1.4	11	8	0965V9	0965V9 laudakia st
41	4	1.4	11	8	0965V6	0965V6 phynocoepta
42	4	1.4	11	8	0965V3	0965V3 phynocoepta
43	4	1.4	11	8	096356	096356 agama atra.
44	4	1.4	11	8	096350	096350 tirapelus sa
45	4	1.4	11	8	0962N4	0962N4 laudakia sa
						0962N4 chlamydosau

ALIGNMENTS

RESULT 1

ID 09R5T6 PRELIMINARY: PRT: 10 AA.

AC 09R5T6; 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)

OS PILIN.

OC Aeromonas sobria.

OC Bacteria; Proteobacteria; gamma subdivision; Aeromonadaceae;

OC Aeromonas.

OX NCBI_TaxID=646;

RN [1]

RP SEQUENCE.

RX MEDLINE=91372953; PubMed=1680105;

RA Hokama A., Iwanaga M.;

RT "Purification and characterization of Aeromonas sobria pili, a possible colonization factor";

RL Infect. Immun. 59:3478-3483(1991).

SQ SEQUENCE 10 AA; 1143 MW; 4C19F942C72B1057 CRC64;

Query Match 1.8%; Score 5; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 5.6e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 210 LVIVI 214

DB 6 LVIVI 10

RESULT 2

ID 09FUX5 PRELIMINARY: PRT: 14 AA.

AC 09FUX5; 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)

OS WAXY (FRAGMENT).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; euasterids II; Dipsacales; Caprifoliaceae; Symphoricarpos.
 OX NCBI_TaxID=13702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Gould K.R., Donoghue M.J.;
 RT "Phylogeny and biogeography of Triosteum (Caprifoliaceae).";
 RL Harv. Pap. Bot. 5:157-166(2000).
 DR EMBL: AF277633; AAC31453.1;
 FT NON_TER 1
 SO SEQUENCE 14 AA; 1485 MW; DD8E2065B7F8E5D CRC64;

Query Match 1.8%; Score 5; DB 10; Length 14;
 Best Local Similarity 100.0%; Pred. No. 7.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 256 EALQA 260
 DB 10 EALQA 14

RESULT 3
 ID Q9RA13 PRELIMINARY; PRT; 16 AA.
 AC Q9RA13;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE MLP SUBUNIT (FRAGMENT).
 OS Mycobacterium leprae.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1769;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96090101; PubMed=7581267;
 RA Deshpande R.G., Khan M.B., Bhat D.A., Navalkar R.G.;
 RT "Immunofluorescence chromatographic isolation of a high molecular weight
 seroreactive protein from Mycobacterium leprae cell sonicate.";
 RL FEMS Immunol. Med. Microbiol. 11:163-169(1995).
 SO SEQUENCE 16 AA; 1842 MW; 54A9ECCA5044F83E CRC64;

Query Match 1.8%; Score 5; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 8.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 DVLRL 23
 DB 6 DVLRL 10

RESULT 4
 ID Q9RS64 PRELIMINARY; PRT; 17 AA.
 AC Q9RS64;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE PILIN (FRAGMENT).
 OS Aeromonas sobria.
 OC Bacteria; Proteobacteria; gamma subdivision; Aeromonadaceae;
 OC Aeromonas.
 OX NCBI_TaxID=646;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93018994; PubMed=1357078;
 RA Iwanaga M., Hokama A.;
 RT "Characterization of Aeromonas sobria TAP13 pili: a possible new
 colonization factor";
 RL J. Gen. Microbiol. 138:1913-1919(1992).
 SO SEQUENCE 17 AA; 1869 MW; 60A8BF85B5E6B236C CRC64;

Query Match 1.8%; Score 5; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 8.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 210 LVIVI 214
 DB 6 LVIVI 10

RESULT 5
 ID P82671 PRELIMINARY; PRT; 17 AA.
 AC P82671;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE THYLAKOID LUMENAL 9 KDA PROTEIN (P9) (FRAGMENT).
 OS Spinacia oleracea (Spinach).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
 OX NCBI_TaxID=3362;
 RN [1]
 RP SEQUENCE.
 RA Kieselbach T., Petersson U., Bystedt M., Schroeder W.P.;
 RL Submitted (MAY-2000) to the SWISS-PROT data bank.
 CC -1 SUBCELLULAR LOCATION: CHLOROPLAST THYLAKOID MEMBRANE LUMEN.
 KW Chloroplast; Thylakoid membrane.
 FT NON_TER 17
 SO SEQUENCE 17 AA; 1683 MW; A8B04C2AEFBDCC1 CRC64;

Query Match 1.8%; Score 5; DB 10; Length 17;
 Best Local Similarity 100.0%; Pred. No. 8.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 FLSGS 209
 DB 2 FLSGS 6

RESULT 6
 ID Q9RSB9 PRELIMINARY; PRT; 20 AA.
 AC Q9RSB9;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE PILIN (FRAGMENT).
 OS Aeromonas sobria.
 OC Bacteria; Proteobacteria; gamma subdivision; Aeromonadaceae;
 OC Aeromonas.
 OX NCBI_TaxID=646;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93225795; PubMed=1363704;
 RA Hokama A., Iwanaga M.;
 RT "Purification and characterization of Aeromonas sobria Ae24 pili: a
 possible new colonization factor.";
 RL Microb. Pathog. 13:325-334(1992).
 SO SEQUENCE 20 AA; 2171 MW; 38BE2BE0A8BF885E CRC64;

Query Match 1.8%; Score 5; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 210 LVIVI 214
 DB 6 LVIVI 10

```

RESULT 7
ID 09T219 PRELIMINARY: PRT: 20 AA.
AC 09T219:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE 14 KDA PHOTOSYSTEM I PSAE PROTEIN (FRAGMENT).
OS Nicotiana sylvestris (Wood tobacco).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
RN NCBI_TaxID=4096;
RN [1]
RP SEQUENCE.
RX MEDLINE=94105345; PubMed=8278548;
RA Obokata J., Mikami K., Hayashida N., Nakamura M., Sugiyama M.;
RT "Molecular heterogeneity of photosystem I. psab, psae, psaf, psah, and
PSL are all present in isoforms in Nicotiana spp.";
RL Plant Physiol. 102:1259-1267(1993).
SQ SEQUENCE 20 AA; 1822 MW; A894589439282E5D CRC64;

Query Match 1.8%; Score 5; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 248 AEGEA 252
DB 14 AEGEA 18

RESULT 9
ID 052266 PRELIMINARY: PRT: 21 AA.
AC 052266:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)

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```

DE PLASMID pBC16 (FROM B. THURINGIENSIS) TETRACYCLINE RESISTANCE (TET)
DE (FRAGMENT).
OS Bacillus thuringiensis.
OC Plasmid pBC16.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
RN NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90253151; PubMed=2160219;
RA Mettus A.M., Macaluso A.;
RT "Expression of Bacillus thuringiensis delta-endotoxin genes during
RT vegetative growth.";
RL Appl. Environ. Microbiol. 56:1128-1134(1990).
DR EMBL: M34478; AAA98049.1; -.
KW Plasmid.
FT NON_TER
SQ SEQUENCE 21 AA; 2489 MW; D93B25AFDC4D8CA6 CRC64;

Query Match 1.8%; Score 5; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 186 SWLYT 190
DB 6 SWLYT 10

RESULT 10
ID 094374 PRELIMINARY: PRT: 24 AA.
AC 094374:
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PPI-LIKE SER/THR PROTEIN PHOSPHATASE (FRAGMENT).
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
RN NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Zeke T., Gergely P., Dombradi V.;
RL Submitted (JUL-1996) to the EMBL/Genbank/DBJ databases.
CC -I- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN +
CC ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).
CC -I- SIMILARITY: TO SERINE/THREONINE SPECIFIC PROTEIN PHOSPHATASE (OR
CC PPP) FAMILY.
DR EMBL: Z77735; CAB01294.1; -.
DR HSSP: P08129; IEFM.
DR InterPro: IPR000934; Ser_thr_phosphatase.
DR Pfam: PF00149; Stryphosphatase; 1.
KW Hydrolase; Iron; Manganese.
FT NON_TER
FT NON_TER
SQ SEQUENCE 24 AA; 2787 MW; F5418DAB76703E54 CRC64;

Query Match 1.8%; Score 5; DB 5; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 DVLRL 23
DB 4 DVLRL 8

RESULT 11
ID 09R4B4 PRELIMINARY: PRT: 25 AA.
AC 09R4B4:
DT 01-MAY-2000 (TREMBLrel. 13, Created)

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DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, last annotation update)
 DE PILIN (FRAGMENT).
 OS Aeromonas trota.
 OC Bacteria; Proteobacteria; gamma subdivision; Aeromonadaceae;
 OX Aeromonas.
 RN NCBI_TaxID=653;
 FT [1]
 RP MEDLINE=97086510; PubMed=8932704;
 RA Nakasone N., Iwanaga M., Yamashiro T., Nakashima K., Albert M.J.,
 RT "Aeromonas trota strains, which agglutinate with Vibrio cholerae O139
 RT Bengal antiserum, possess a serologically distinct fimbrial
 RT colonization factor."
 RL Microbiology 142:309-313(1996).
 SO SEQUENCE 25 AA; 2697 MW; BFCABF6292A8A533 CRC64;

Query Match 1.8%; Score 5; DB 2; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 210 LVYVI 214
 |||||
 DB 6 LVYVI 10

RESULT 12
 ID 014497 PRELIMINARY; PRT; 25 AA.
 AC 014497;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
 DE 01-NOV-1996 (TREMBLrel. 01, last annotation update)
 DE CCAAT BINDING FACTOR SUBUNIT C (FRAGMENT).
 GN HCBF-C.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRIN;
 RA Dmitrenko V.V., Garifullin O.M., Shostak K.A., Smukodub A.I.,
 RA Kaysan V.M.;
 RL Submitted (MAR-1996) to the EMBL/genbank/DBD databases.
 DR EMBL: 270024; CAA93846.1; -.
 FT NON_TER 25
 FT SEQUENCE 25 AA; 2649 MW; 12DE150C48C31875 CRC64;

Query Match 1.8%; Score 5; DB 4; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 GTSSS 199
 |||||
 DB 9 GTSSS 13

RESULT 13
 ID 09N029 PRELIMINARY; PRT; 25 AA.
 AC 09N029;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
 DE 01-OCT-2000 (TREMBLrel. 15, last annotation update)
 DE ARYHYDROCARBON RECEPTOR (FRAGMENT).
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Bartol F.F., Hillman L.A., Wiley A.A., Mower J., Tarleton B.J.;
 RT "Arylhdrocarbon Receptor (Ahr) Expression in the Porcine Uterus."
 RL Biol. Reprod. 0:0-0(2000).
 DR EMBL: AF233432; AAF43428.1; -.
 KW Receptor.
 FT NON_TER 25
 FT SEQUENCE 25 AA; 2648 MW; 267602488DE5B276 CRC64;

Query Match 1.8%; Score 5; DB 6; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 226 KRRKP 230
 |||||
 DB 14 KRRKP 18

RESULT 14
 ID 0910R5 PRELIMINARY; PRT; 25 AA.
 AC 0910R5;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
 DE 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE REV PROTEIN (FRAGMENT).
 GN REV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PATIENT 1;
 RX MEDLINE=20338596; PubMed=10881687;
 RA Yamada T., Iwamoto A.;
 RT "Comparison of proviral accessory genes between long-term
 RT nonprogressors and progressors of human immunodeficiency virus type 1
 RT infection."
 RL Arch. Virol. 145:1021-1027(2000).
 DR EMBL: AB034363; BAA93826.1; -.
 DR InterPro: IPR000625; REV.
 DR Pfam: PF00424; REV; 1.
 FT NON_TER 25
 FT SEQUENCE 25 AA; 2682 MW; 1F922P59A1CP2758 CRC64;

Query Match 1.8%; Score 5; DB 12; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 218 TVGLI 222
 |||||
 DB 15 TVGLI 19

RESULT 15
 ID 071988 PRELIMINARY; PRT; 25 AA.
 AC 071988;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
 DE 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE PATIENT 3799(12-88), CLONE 33 ACCESSORY REGION GENES, CDS (FRAGMENT).
 GN REV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PATIENT 3799(12-88);
 RX MEDLINE=95287475; PubMed=7769682;
 RA Michael N.L., Chang G., d'Arcy L.A., Ehrenberg P.K., Mariani R.,

RA Busch M.P., Birx D.L., Schwartz D.H.;
 RT "Defective accessory genes in a human immunodeficiency virus type 1-
 infected long-term survivor lacking recoverable virus.";
 RL J. VIROL. 69:428-436(1995).
 DR EMBL; U24481; AAA79642.1; -;
 DR InterPro; IPR000625; REV.
 DR Pfam; PF00424; REV; 1.
 FT NON_TER 25
 SQ SEQUENCE 25 AA; 2744 MW; 1F922F59A5DF261D CRC64;

Query Match 1.8%; Score 5; DB 12; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 218 TVGLI 222
 |||||
 Db 15 TVGLI 19

Search completed: January 24, 2002, 16:29:00
 Job time: 190 sec

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PR 27-APR-1995; 95WO-US05058.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Gentz R, Ni J, Rosen CA;
XX
XX WPI; 1996-497627/49.
DR N-PSDB; AAT40048.
XX
XX New nucleic acid encoding a human tumour necrosis factor receptor -
PT useful for treatment of auto-immune diseases etc., in diagnosis and
PT for drug screening
XX
XX Claim 1; Pages 47-48; 73pp; English.
XX
XX The present sequence is the human tumour necrosis factor (TNF)
CC receptor, which may be used for the identification of TNF receptor
CC agonists or antagonists. TNF receptor agonists inhibit tumour
CC growth, stimulate cell (e.g. T cell) differentiation, mediate the
CC immune and antiviral responses, regulate growth, protect against
CC radiation and Chlamydia infection, and can be used to treat
CC immunodeficiencies, e.g. human immunodeficiency virus. Antagonists
CC can be used to treat T cell mediated autoimmune disease.
CC inflammation, septic shock, cerebral malaria, cachexia or B cell
CC cancers, to inhibit graft-host reactions and to prevent apoptosis
CC or cytotoxicity. Fragments of the TNF receptor encoding DNA can be
CC used as hybridisation probes for detecting related genes.
CC Antibodies against the protein can be used as reagents for
CC detecting/measuring soluble forms of protein in the circulation.
XX
XX Sequence 283 AA:
SQ

```

Query Match 100.0%; Score 1578; DB 17; Length 283;
 Best Local Similarity 100.0%; Pred. No. 4.5e-121;
 Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 MEPPGDMGPPMWRSPRTDVLRLVLYLTFLGAPCYAPALPSCKEDEYPVSGCCPKCSPG 60
DB 1 meppgdmgppmwrsprrtdvrlvlyltflgapecyapalpsckedeypyvgsecpcpspg 60
OY 61 YRKKEAGELGTGVCPCPPGTYIAHLNGLSKLCQOMCDPAMGLRASRNCSTENAVCG 120
DB 61 yrkkeageltgtvcpcppgyiahlnglskclqcmcdpanglrasrncstenaavcg 120
OY 61 yrkkeageltgtvcpcppgyiahlnglskclqcmcdpanglrasrncstenaavcg 120
DB 61 yrkkeageltgtvcpcppgyiahlnglskclqcmcdpanglrasrncstenaavcg 120
OY 121 CSPGHFCIVQDDGHCACRAVATSSPGORVQKGTESODTLQNCPPGTSPNGTLEECQ 180
DB 121 cspghfcivqddghcaacrayatsspgqrvqkygtesqdtlqncppgtspngtleecq 180
OY 181 HOTKCSMLVTKAGAGTSSSHWMMFLSGSLVIYVCSVGLIICVRRKPRGQDVAVKIVS 240
DB 181 hotkcsmlvtkagagtssshwmmflsgslviyvcstvglllcvtrrprgqdvavkivs 240
OY 241 VQKRGAEAEATVIALQAPPDVTTVAVEETIPSTGSPNH 283
DB 241 vqkrgaeaeatvialqapppvtlvaveetipstgrspnh 283

```

RESULT: 2
 AAM69238 standard; Protein; 283 AA.
 AAM69238;
 21-OCT-1998 (first entry)
 Herpesvirus entry mediator protein.
 Entry mediator gene; herpesvirus; HVEM; tumour necrosis factor receptor;
 gene expression regulator; cellular stress; inflammatory response;
 lymphocyte activity regulator; autoimmune response.
 Homo sapiens.

```

XX
XX MO9825967-AI.
PN
XX 18-JUN-1998.
PD
XX
XX 05-DEC-1997; 97WO-US22278.
PF
XX
XX 12-DEC-1996; 96US-0032705.
PR
XX
XX (GETH ) GENENTECH INC.
PA
XX Ashkenazi AJ, Marsters SA;
XX PI
XX
XX WPI; 1998-348457/30.
DR N-PSDB; AAV44852.
XX
XX Herpesvirus entry mediator polypeptide, HVEM - useful, e.g. in
PT assays for HVEM and to produce antibodies and transgenic animals,
PT e.g. for drug screening
XX
XX Claim 1; Fig 1; 46pp; English.
XX
XX This sequence is the herpesvirus entry mediator (HVEM) protein of
CC the invention. The protein is useful in quantitative diagnostic assays
CC for HVEM, in affinity purification of HVEM from recombinant cells/natural
CC sources and in competitive-type receptor binding assays. It can also be
CC used to generate antibodies, also useful in diagnostic assays for HVEM
CC and affinity purification of HVEM. HVEM is believed to be a member of the
CC tumour necrosis factor receptor (TNFR) family, and transient transfection
CC of HVEM into human 293 cells caused marked activation of certain
CC transcription factors, e.g. AP-1, suggesting that HVEM is involved in
CC regulating gene expression in response to infectious stimuli and cellular
CC stress. The predominant expression of HVEM mRNA in lymphocyte-rich
CC tissues (e.g. spleen and peripheral blood) also suggested it may be a
CC receptor in regulating lymphocyte activity. Antibodies produced may be
CC therefore be useful therapeutically, e.g. antagonistic antibodies may be
CC useful to block excessive inflammatory/autoimmune response resulting from
CC e.g. AP-1 induction, whilst agonistic antibodies may enhance HVEM
CC regulation of such induction. The DNA may be used diagnostically, e.g.
CC to determine if DNA and/or RNA encoding HVEM is present in cells, and to
CC prepare HVEM polypeptide recombinantly. It is also useful to produce
CC non-human transgenic animals (e.g. mice or rats), especially knockout
CC animals containing cells with an altered gene encoding HVEM polypeptide.
CC Such animals are useful in the development and screening of
CC therapeutically useful reagents.
XX
XX Sequence 283 AA:
SQ

```

Query Match 100.0%; Score 1578; DB 19; Length 283;
 Best Local Similarity 100.0%; Pred. No. 4.5e-121;
 Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

OY 1 MEPPGDMGPPMWRSPRTDVLRLVLYLTFLGAPCYAPALPSCKEDEYPVSGCCPKCSPG 60
DB 1 meppgdmgppmwrsprrtdvrlvlyltflgapecyapalpsckedeypyvgsecpcpspg 60
OY 61 YRKKEAGELGTGVCPCPPGTYIAHLNGLSKLCQOMCDPAMGLRASRNCSTENAVCG 120
DB 61 yrkkeageltgtvcpcppgyiahlnglskclqcmcdpanglrasrncstenaavcg 120
OY 61 yrkkeageltgtvcpcppgyiahlnglskclqcmcdpanglrasrncstenaavcg 120
DB 61 yrkkeageltgtvcpcppgyiahlnglskclqcmcdpanglrasrncstenaavcg 120
OY 121 CSPGHFCIVQDDGHCACRAVATSSPGORVQKGTESODTLQNCPPGTSPNGTLEECQ 180
DB 121 cspghfcivqddghcaacrayatsspgqrvqkygtesqdtlqncppgtspngtleecq 180
OY 181 HOTKCSMLVTKAGAGTSSSHWMMFLSGSLVIYVCSVGLIICVRRKPRGQDVAVKIVS 240
DB 181 hotkcsmlvtkagagtssshwmmflsgslviyvcstvglllcvtrrprgqdvavkivs 240
OY 241 VQKRGAEAEATVIALQAPPDVTTVAVEETIPSTGSPNH 283
DB 241 vqkrgaeaeatvialqapppvtlvaveetipstgrspnh 283

```

```

RESULT 3
AA06488
ID AAY06488 standard: Protein; 263 AA.
XX
AC AAY06488;
XX
DT 27-SEP-1999 (first entry)
XX
DE Human tumour-associated protein PRO509.
XX
KW PRO112; UNQ555; cancer; tumour necrosis factor receptor;
diagnosis; therapy; human.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 201..225
FT /note= "transmembrane domain"
FT 226..283
FT /note= "cytoplasmic domain"
XX
PN W09935170-A2.
XX
PD 15-JUL-1999.
XX
PE 05-JAN-1999; 99WO-US00106.
XX
PR 20-NOV-1998; 98US-0109304.
PR 05-JAN-1998; 98US-0070440.
PR 29-APR-1998; 98US-0083500.
PR 22-MAY-1998; 98US-0086414.
PR 10-JUN-1998; 98US-0088742.
PR 10-NOV-1998; 98US-0107783.
XX
PA (GENE) GENENTECH INC.
XX
PI Botstein D, Goddard A, Gurney AL, Hillan KJ, Lawrence DA;
PI Roy MA, Wood WI;
XX
DR WPI: 1999-430385/36.
DR N-PSDB: AAX87265.
XX
PT Antibody against proteins expressed in neoplastic cells, useful for
tumor diagnosis and treatment
XX
PE Example 1; Fig 24; 162pp; English.
XX
CC This sequence represents human PRO509 (UNQ329), a protein encoded
by the novel cDNA clone DNA50148 (see AAX87264), and a member of the
tumor necrosis factor receptor family. Amplification of DNA50148
was observed in various tumour tissues, suggesting a role in tumour
formation or growth. Antagonists (e.g. antibodies) directed to
PRO509 may have use in cancer therapy. The invention identifies
14 genes (see AAX87254-67) that are amplified in the genome of tumour
cells. Such amplification is expected to be associated with
overexpression of the gene product and to contribute to tumorigenesis.
CC The encoded proteins (see AAY06477-90) may be useful targets for the
diagnosis and/or treatment (including prevention) of certain cancers,
and may act as predictors of the prognosis of tumour treatment.
CC Antibodies that bind the proteins are claimed and used in claimed
cancer diagnostic kits.
XX
SQ Sequence 283 AA;

```

```

Query Match 100.0%; Score 1578; DB 20; Length 283;
Best Local Similarity 100.0%; Pred. No. 4; 5e-121; Indels 0; Gaps 0;
Matches 283; Conservative 0; Mismatches 0;
1 MBPQDMDGPPWRSTPRDVLRLVLTFLGAPCYAPALPSCKEDEYVGSCECPKCSPG 60
|||||
1 mpppdpwppprstprtdvlrlvltflgapyapalpsckedeypvgsccpckspg 60

```

```

RESULT 4
AAY94721
ID AAY94721 standard: Protein; 263 AA.
XX
AC AAY94721;
XX
DT 29-JAN-2001 (first entry)
XX
DE Human TR2-receptor protein sequence.
XX
KW Tumour necrosis factor-receptor related protein; TR2; human; cancer;
chromosome p36.2-p36.3; arthritis; inflammation; autoimmune disease;
immunodeficiency; metastasis; haemolytic anaemia; asthma; X-linked SCID;
severely combined immunodeficiency; apoptosis inhibition;
Alzheimer's disease; Parkinson's disease; Crohn's disease.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..38
FT /note= "Signal peptide"
FT Protein 39..283
FT /label= "TR2 receptor"
XX
PN W020056405-A2.
XX
PD 28-SEP-2000.
XX
PE 22-MAR-2000; 2000WO-US07521.
XX
PR 22-MAR-1999; 99US-0125683.
PR 26-MAR-1999; 99US-0126522.
PR 20-MAY-1999; 99US-0135169.
PR 06-AUG-1999; 99US-0147383.
XX
PA (NIDJ) NI J.
PA (ROSE) ROSEN C A.
PA (GENTZ) GENTZ R L.
XX
PI NI J, Rosen CA, Gentz RL;
XX
DR WPI: 2000-594519/56.
DR N-PSDB: AAA28149.
XX
PT Nucleic acid molecule encoding a human tumor necrosis factor receptor 2
and its two splice variants, useful for treating arthritis or
inflammation, cancer (such as follicular lymphomas) and
immunodeficiency disorders -
XX
PS Disclosure: Page 370: 373pp: English.
XX
CC This invention relates to an isolated nucleic acid molecule encoding a
human tumor necrosis factor(TNF)-receptor related protein TR2. Included
in the invention are the two splice variants of TR2, TR2-SV1 and TR2-SV2.
CC The TR2 gene is located on chromosome 1 at position p36.2-p36.3. TR2 is a

```


Db 1 meppgdwpppwrstprtdvrlvlylftlfgapcyapalpsckedeyvvgsecpcpspg 60
Qy 61 YRVKACGELTGTVCCEPCPGTYIAHLNGLSKLOCMCDPMAGIRASRNCSTENAVCG 120
Db 61 yrvkacgelgtvcepcpgtyiahlnglskclqcmcdpamgirasrncstenavcg 120
Qy 121 CSPGHFCIVODGDHCAACRAVATSSPGORVOKGTESDDTLCQNCPPGTFSPNGTLEECQ 180
Db 121 cspghfcivodgdhcaacraatsspggrvqkgtesqdtlccqncppgtfispngtleecq 180
Qy 181 HQFKCSMLVTRKAGAGTSSSHWWMFLSGSLVIVIVCSTVGLLICVKRRKPRGDDVVKVIVS 240
Db 181 hqtkcsmlvtrkagagtssshwwmflsgslviviavcstvglllcvkrrkprgddvkvivs 240
Qy 241 VQKRROAEAGETVIEALQAPPDVTVAVEETIPSTGSRPNH 283
Db 241 vqkrroaeagetvlealqappdvltvaaveetlpsitgrspnh 283

RESULT 6

AA95348 ID AAY95348 standard; Protein: 283 AA.

AA95348; AC XX

DT 25-SEP-2000 (first entry)

DE Human PRO509 antitumour protein.

KW PRO509; human; antitumour; tumour; therapy; cytostatic;
uterine cancer; ovarian cancer; renal cancer; colorectal cancer;
central nervous system cancer; melanoma; leukaemia; neoplasm.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..36 /label= Signal_peptide

FT Protein 37..283 /label= PRO509

FT Domain 205..221 /note= "transmembrane domain"

FT Modified-site 81..87 /note= "N-myristoylation"

FT Modified-site 89..95 /note= "N-myristoylation"

FT Modified-site 104..110 /note= "N-myristoylation"

FT Modified-site 120..126 /note= "N-myristoylation"

FT Modified-site 153..159 /note= "N-myristoylation"

FT Modified-site 193..199 /note= "N-myristoylation"

FT Modified-site 192..201 /note= "N-myristoylation"

FT Modified-site 220..226 /note= "N-myristoylation"

FT Modified-site 110..114 /note= "N-myristoylation"

FT Modified-site 173..177 /note= "Asn is N-glycosylated"

FT Region 231..234 /note= "Asn is N-glycosylated"

XX MO200037638-A2.

PD 29-JUN-2000.

XX 02-DEC-1999; 99WO-US28565.

PR 22-DEC-1998; 98US-0113296.
PR 08-MAR-1999; 99WO-US05028.
PR 21-APR-1999; 99US-0130232.
PR 28-APR-1999; 99US-0131445.
PR 14-MAY-1999; 99US-0134287.
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
XX (GETH) GENENTECH INC.
XX Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Marsters SA;
PI Napier MA, Pittl RM, Wood WI;
XX WPI: 2000-442668/38.
XX N-PSDB: AAA45727.
XX Novel composition to inhibit neoplastic cell growth or for treating
PT tumor in mammal comprises polypeptides PRO179, PRO207, PRO320, PRO219,
PT PRO221, PRO224, PRO328, PRO301, PRO526, PRO362, PRO356, PRO509 or
PT PRO866
XX Claim 19; Fig 24; 172pp; English.

XX The present sequence is that of human antitumour protein PRO509,
CC as deduced from a retinal cDNA clone (see AAA49727). PRO509 shows
CC homology to members of the human tumour necrosis factor receptor
CC family such as the lymphotoxin-beta receptor (11 identities) and
CC CD40 (12 identities). A claimed method for inhibiting the growth
CC of a tumour cell comprises exposing the tumour cell to PRO179,
CC PRO207, PRO320, PRO219, PRO224, PRO328, PRO301, PRO526,
CC PRO362, PRO356, PRO509 or PRO866 (see AAY95337-49), their agonists or
CC chimeric polypeptides incorporating them. The tumour is especially
CC a cancer selected from breast, ovarian, renal, colorectal, uterine,
CC prostate, lung, bladder and central nervous system cancer, melanoma
CC and leukaemia. Methods for the recombinant expression of the
CC antitumour proteins are also provided.

XX Sequence 283 AA:

Query Match 100.0%; Score 1578; DB 21; Length 283;
Best Local Similarity 100.0%; Pred. No. 4.5e-121;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPPGDWGPpPWRSTPRtdVRLVlyLftlFGAPCYAPALpSCkEDEYVvgSECCpKcSPG 60
Db 1 meppgdwgpPPwrstprtdvrlvlylftlfgapcyapalpsckedeyvvgsecpcpspg 60
Qy 61 YRVKACGELTGTVCCEPCPGTYIAHLNGLSKLOCMCDPMAGIRASRNCSTENAVCG 120
Db 61 yrvkacgelgtvcepcpgtyiahlnglskclqcmcdpamgirasrncstenavcg 120
Qy 121 CSPGHFCIVODGDHCAACRAVATSSPGORVOKGTESDDTLCQNCPPGTFSPNGTLEECQ 180
Db 121 cspghfcivodgdhcaacraatsspggrvqkgtesqdtlccqncppgtfispngtleecq 180
Qy 181 HQFKCSMLVTRKAGAGTSSSHWWMFLSGSLVIVIVCSTVGLLICVKRRKPRGDDVVKVIVS 240
Db 181 hqtkcsmlvtrkagagtssshwwmflsgslviviavcstvglllcvkrrkprgddvkvivs 240
Qy 241 VQKRROAEAGETVIEALQAPPDVTVAVEETIPSTGSRPNH 283
Db 241 vqkrroaeagetvlealqappdvltvaaveetlpsitgrspnh 283

RESULT 7

AA60045 ID AAW60045 standard; Protein: 283 AA.

AC XX AAW60045;

XX

Qy	121	CSFGRHCTIVQDDDHCKACACATATSSGQAVQKGTSDTLOQNCPRGTFSPAGTLEEQ	180
Db	121	csfgrhctivqdddhckacacatatsspgqvqkygtesqdtlcncppgltfspngtleeq	180
Qy	181	HOTKCSMLVTKAGAGTSSSHWMMFLSGSLVIVYICSTVGLITICVRRRPRGDIYAVIS	240
Db	181	hqtktcswlvtkagagssshwmmflsgslvlyivestvlglllcvtirrpgrdvavivis	240
Qy	241	VQRKROAEGEATVIFALQAPPDVTVVAEETIPSTGRSPNH	283
Db	241	vqkrqaegeatvlealqappdvttvaveetipstfgrspnh	283
RESULT 8			
ID	AAW87591	standard; Protein: 283 AA.	
AC	AAW87591;		
XX			
XX	17-MAR-1999	(first entry)	
DT			
XX			
DE		Human tumour necrosis factor receptor-like 2 protein.	
XX			
KW		Tumour necrosis factor receptor-like 2; TR2; TNF; human; psoriasis;	
KW		systemic lupus erythematosus; idiopathic thrombocytopenic purpura;	
KW		rheumatoid arthritis; multiple sclerosis; inflammatory bowel disease;	
KW		insulin-dependent diabetes mellitus; allergic disorder; cancer; therapy;	
KW		arteriosclerosis; viral infection.	
XX			
OS		Homo sapiens.	
XX			
PN	WO9851346-A1.		
XX			
PD	19-NOV-1998.		
XX			
PF	12-MAY-1998; 98WO-0509744.		
XX			
PR	12-MAY-1997; 97US-0046249.		
XX			
PA	(SMIK) SMITHKLINE BEECHAM CORP.		
XX	(SMIK) SMITHKLINE BEECHAM PLC.		
PI	Harrop JA, Holmes SD, Reddy MP, Truneh A;		
XX			
DR	WPI: 1999-059689/05.		
XX	N-PSDB: AAW83763.		
PT		Method of treating pathological condition - comprises administering	
XX		tumour necrosis factor-2 antibody to patient	
PS		Disclosure: Page 27-28; 35pp; English.	
XX			
CC		This sequence represents the human tumour necrosis factor (TNF)	
CC		receptor-like 2 (TR2) protein. Antibodies that target the TR2 protein can	
CC		be used in the method of the invention to treat pathological conditions.	
CC		The method is used to treat systemic lupus erythematosus, idiopathic	
CC		thrombocytopenic purpura, rheumatoid arthritis, multiple sclerosis,	
CC		psoriasis, inflammatory bowel disease, insulin-dependent diabetes	
CC		mellitus, allergic disorders, e.g. asthma, allergic rhinitis and atopic	
CC		dermatitis, cancer, e.g. lymphomas and leukemias, arteriosclerosis and	
CC		viral infections, e.g. Herpes simplex virus and AIDS. The TR2 antibody	
CC		is also used to monitor and diagnose abnormalities in TR-2 function,	
CC		production or metabolism.	
XX			
SO	Sequence	283 AA:	
Query Match 99.8%; Score 1575; DB 20; Length 283;			
Best Local Similarity 99.6%; Pred. No. 8e-121;			
Matches 282; Conservative 1; Mismatches 0; Indels 0; Gaps 0;			
1 MPPGDGWPMPRSTPTDVLRLVLYLFLGAPCYAPALPSCDEDEYVSGECPCKCSFG 60			

Db 1 mepgwdwppwrsbtktdvrlvlyltflgapcyapalpsckedeyvsgccpkcspg 60
 OY 61 YRVKACGELTGTCEPCPPGTIYAHNLGSKLCQCMCDPAMGLRASRNCSTRNAYCG 120
 Db 61 yrvkeacgelgtvcepcppgtiyahnlgsklcqcmcdpamglrasrncstrnacyg 120
 OY 121 CSPGHFCIVODGDHCAACRAVATSSPGORVKGESODTLCQNCPPGTFSPNGTLEECQ 180
 Db 121 cspghfcivodgdhcaacrayatspgqrvkgtesqdtlcqncppgtfspngtleecq 180
 OY 181 HOTKCSMLVTRKAGACTSSSHWWMFLSGSLVIVYVSTVGLIICVKKRRKPGDVVKIVS 240
 Db 181 hgtkcsmlvtrkagactssshwwmflsgslviviycstvglllcvkrrkpgdvvkivls 240
 OY 241 VQRKROAEAGATVTEALQAPPDVTVAVEETIPSEFGRSPNH 283
 Db 241 vqkrroaeagatvtealqappdvltvaeetlpsfgrspnh 283

RESULT 9
 AAY94717
 ID AAY94717 standard; Protein: 283 AA.
 AC AAY94717;
 DT 29-JAN-2001 (first entry)
 XX
 DE Human TR2-receptor protein sequence.
 XX
 KW Tumour necrosis factor-receptor related protein; TR2; human; cancer;
 KW chromosome p36.2-p36.3; arthritis; inflammation; autoimmune disease;
 KW immunodeficiency; metastasis; haemolytic anaemia; asthma; X-linked SCID;
 KW severely combined immunodeficiency; apoptosis inhibition;
 KW Alzheimer's disease; Parkinson's disease; Crohn's disease.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..36
 FT Protein /note="Signal peptide"
 FT Domain /label="TR2 receptor"
 FT Domain /note="37..200"
 FT Domain /note="Extracellular domain"
 FT Domain /note="201..225"
 FT Domain /note="Transmembrane domain"
 FT Domain /note="226..283"
 FT Domain /note="Intracellular domain"
 XX
 PN WO200056405-A2.
 PD 28-SEP-2000.
 PF 22-MAR-2000; 2000WO-US07521.
 XX
 XX 22-MAR-1999; 99US-0125683.
 PR 26-MAR-1999; 99US-0126522.
 PR 20-MAY-1999; 99US-0135169.
 PR 06-AUG-1999; 99US-0147383.
 XX
 PA (NIJ/J) NI J.
 PA (ROSE/) ROSEN C A.
 PA (GENT/) GENTZ R L.
 PI NI J, Rosen CA, Gentz RL.
 XX
 DR WPI: 2000-594519/56.
 DR N-PSDB: AAA28135.
 XX
 PT Nucleic acid molecule encoding a human tumor necrosis factor receptor 2
 PT and its two splice variants, useful for treating arthritis or
 PT inflammation, cancer (such as follicular lymphomas) and
 PT immunodeficiency disorders -

XX
 PS Claim 1; Fig 1; 373pp; English.
 CC
 CC This invention relates to an isolated nucleic acid molecule encoding a
 CC human tumor necrosis factor (TNF)-receptor related protein TR2. Included
 CC in the invention are the two splice variants of TR2, TR2-SV1 and TR2-SV2.
 CC The TR2 gene is located on chromosome 1 at position p36.2-p36.3. TR2 is a
 CC member of the TNFR superfamily. The invention includes a method for the
 CC treatment of arthritis or inflammation using an antibody directed against
 CC a fragment of the TR2 protein. TR2 its agonists, antagonists and
 CC antibodies exhibit cytostatic, dermatological, antianemic,
 CC immunosuppressive, antiallergic, antiarthritic, antiasthmatic,
 CC antineoplastic, neuroprotective, nootropic, antiparkinsonian, and
 CC cerebroprotective activity. The methods are useful for treating arthritis
 CC or inflammation, cancer (such as follicular lymphomas, carcinoma with p53
 CC mutations, cardiac tumors, pancreatic, breast, or prostate cancer), an
 CC immunodeficiency or for enhancing an in vivo leukocyte response to an
 CC antigen. Anti-TR2 antibodies are useful for treating, inhibiting or
 CC preventing autoimmune diseases (such as autoimmune haemolytic anaemia,
 CC dermatitis, allergic encephalomyelitis, rheumatoid arthritis, asthma, and
 CC inflammatory myopathies) and immunodeficiency disorders (such as severely
 CC combined immunodeficiency (SCID)-X linked, B cell lymphoproliferative
 CC disorder, or Nezelof syndrome-combined immunodeficiency with 19s). TR2,
 CC TR2-SV1 and/or TR2-SV2 polynucleotides and polypeptides, agonists or
 CC antagonists are useful for treating or preventing autoimmune diseases and
 CC inhibit the growth, progression and/or metastasis of cancers. They are
 CC also used to activate, differentiate or proliferate cancerous cells or
 CC tissues, and can be used to treat diseases associated with increased cell
 CC survival, or the inhibition of apoptosis, e.g. Alzheimer's disease,
 CC Parkinson's disease, or Crohn's disease. The TR2 polypeptides are useful
 CC as sources for generating antibodies, as molecular weight markers.
 CC This sequence represents the TR2 receptor protein of the invention.
 XX
 SQ Sequence 283 AA:

Query Match. 99.8%; Score 1575; DB 21; Length 283;
 Best Local Similarity 99.6%; Pred. No. 8e-121;
 Matches 282; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 MPPGDWGPWPWRSTPRTDVLRLVLYLTFLGAPCYAPALPSCKEDEVVSGCCPKCSPG 60
 Db 1 mepgwdwppwrsbtktdvrlvlyltflgapcyapalpsckedeyvsgccpkcspg 60
 OY 61 YRVKACGELTGTCEPCPPGTIYAHNLGSKLCQCMCDPAMGLRASRNCSTRNAYCG 120
 Db 61 yrvkeacgelgtvcepcppgtiyahnlgsklcqcmcdpamglrasrncstrnacyg 120
 OY 121 CSPGHFCIVODGDHCAACRAVATSSPGORVKGESODTLCQNCPPGTFSPNGTLEECQ 180
 Db 121 cspghfcivodgdhcaacrayatspgqrvkgtesqdtlcqncppgtfspngtleecq 180
 OY 181 HOTKCSMLVTRKAGACTSSSHWWMFLSGSLVIVYVSTVGLIICVKKRRKPGDVVKIVS 240
 Db 181 hgtkcsmlvtrkagactssshwwmflsgslviviycstvglllcvkrrkpgdvvkivls 240
 OY 241 VQRKROAEAGATVTEALQAPPDVTVAVEETIPSEFGRSPNH 283
 Db 241 vqkrroaeagatvtealqappdvltvaeetlpsfgrspnh 283

RESULT 10
 AAW95031
 ID AAW95031 standard; protein: 283 AA.
 AC AAW95031;
 DT 13-MAY-1999 (first entry)
 XX
 DE Tumour necrosis factor receptor (TNF-R) related polypeptide TR2.
 XX
 KW Tumour necrosis factor receptor; TNF-R; TR1; TR2; TR4; arthritis;
 KW inflammation; septicemia; autoimmune disease; transplant rejection;

KW graft vs. host disease; infection; stroke; ischemia; brain injury; AIDS;
 KW acute respiratory disease syndrome; restenosis; bone disease; cancer;
 XX atherosclerosis; Alzheimer's disease.
 OS Unidentified.
 XX EP897114-A2.
 XX 17-FEB-1999.
 XX PD
 XX PF 04-JUN-1998; 98EP-0304424.
 XX XX
 XX 29-AUG-1997; 97US-0057550.
 PR 13-AUG-1997; 97US-0055513.
 PR 26-AUG-1997; 97US-0056980.
 XX XX
 XX (SMIK) SMITHKLINE BEECHAM CORP.
 XX Brigham-burke MR, Young PR;
 XX WPI: 1999-134308/12.
 DR
 XX
 PT Identifying agonists and antagonists to tumour necrosis factor
 PT receptor (TNF-R) related polypeptides (TR1, TR2, TL2 and TL4) -
 PT useful for treating stroke, Alzheimer's disease and AIDS
 PT
 PS Disclosure: Page 13-14; 18pp; English.
 XX
 XX The invention relates to identifying agonists or antagonists to tumour
 CC necrosis factor receptor (TNF-R) related polypeptides (TR1 and TR2, TL2
 CC and TL4). The method comprises: (a) (i) contacting TR1 or TR2 with a
 CC candidate compound in the presence of TL2 or TL4; or (ii) contacting TL2
 CC or TL4 with a candidate compound in the presence of TR1 or TR2; and (b)
 CC assessing the ability of the candidate compound to compete with TR1 or
 CC TR2 binding to TL2 or TL4. TR and TL agonists and antagonists are useful
 CC for treating diseases caused by imbalance of TL or TR polypeptide levels,
 CC which cause: chronic and acute inflammation, arthritis, septicemia,
 CC autoimmune diseases, transplant rejection, graft vs. host disease,
 CC infection, stroke, ischemia, acute respiratory disease syndrome,
 CC restenosis, brain injury, AIDS, bone diseases, cancer, atherosclerosis
 CC and Alzheimer's disease. The present sequence represents a TNF-R related
 CC polypeptide TR2.
 CC
 SQ Sequence 283 AA:

Query Match 99.6%; Score 1572; DB 20; Length 283;
 Best Local Similarity 99.6%; Pred. No. 1,4e-120;
 Matches 282; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MEPPGDMGPPMSPRTPTVLRVLVTLFGAPCVAPALPSCKEDEYPVGSECCPSPG 60
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DB 61 YRVKKAAGELTGVCEPPCGTYIAHLNGLSKLQCMQMDPAMGRASRNCSTENAVCG 120
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DB 121 CSPGHGCIYQDDGHCACAGATATSSFGQVQKGTESQTLQCNCPGTFSPNGTLEECQ 180
QY 181 HQTGKSWLTAKAGAGTSSSHWMMFLSGSLVIVYCSYTGILITCYKRRKPRGQVYVITS 240
DB 181 HQTGKSWLTAKAGAGTSSSHWMMFLSGSLVIVYCSYTGILITCYKRRKPRGQVYVITS 240
QY 241 YORRQEAEGEATVIEALQAPPDVTVAVETIPSTFGSPHN 283
DB 241 YORRQEAEGEATVIEALQAPPDVTVAVETIPSTFGSPHN 283

```

RESULT 11
 AAW12659

ID AAW12659 standard; Protein; 283 AA.
 XX AC AAW12659;
 XX XX
 DT 07-MAY-1997 (first entry)
 XX XX
 DE Human herpes simplex virus cellular mediator.
 XX XX
 KW Herpes simplex virus cellular mediator; HVEW; receptor; HSV;
 KW diagnosis; agonist; antagonist; antibody.
 XX XX
 OS Homo sapiens.
 XX XX
 FH Key Location/Qualifiers
 FH Peptide 1..38
 FT /label= Sig-peptide
 FT Protein 39..283
 FT /label= Mat-protein
 FT Region 42..75
 FT /note= "cysteine-rich repeat characteristic of
 FT TNF/NGF receptor family"
 FT Region 76..120
 FT /note= "cysteine-rich repeat characteristic of
 FT TNF/NGF receptor family"
 FT Region 121..162
 FT /note= "cysteine-rich repeat characteristic of
 FT TNF/NGF receptor family"
 FT Region 163..185
 FT /note= "partial cysteine-rich repeat characteristic
 FT of TNF/NGF receptor family"
 FT Domain 203..225
 FT /label= Transmembrane_domain
 FT Modified-site 110..112
 FT /label= Glycosylation
 FT FT /note= "potential N-glycosylation site"
 FT Modified-site 173..175
 FT /label= Glycosylation
 FT FT /note= "potential N-glycosylation site"
 PN W09704658-A1.
 XX PD 13-FEB-1997.
 XX XX
 XX 26-JUL-1996; 96WO-US12374.
 XX PF
 XX 28-JUL-1995; 95US-0509024.
 XX PR
 XX (NOUN) UNIT NORTHWESTERN.
 XX PI Montgomery RI, Spear PG;
 XX DR WPI: 1997-145273/13.
 XX N-PSDB: AAT51737.
 XX XX
 PT New human herpes simplex virus cellular mediator - used for
 PT diagnosis, drug screening and therapeutically to inhibit entry of
 PT HSV into cells
 PT
 PS Claim 1; Fig 2; 54pp; English.
 XX XX
 CC Human herpes simplex virus (HSV) cellular mediator (HVEW) (AAW12659)
 CC is a novel member of the TNF/NGF receptor family that mediates or
 CC enhances entry of HSV into cells. Its amino acid sequence was
 CC deduced from a cDNA clone (AAT51737) isolated from an HeLa library
 CC by its ability to convert CHO-K1 cells from resistance to
 CC susceptibility to HSV-1 entry. Recombinant HVEW can be produced in
 CC bacterial or mammalian (esp. CHO) cells. It can be used as an
 CC immunosay reagent to detect specific antibodies, to screen for
 CC drugs having an (ant)agonist effect on HSV entry into cells, to
 CC generate antibodies, to screen for the (currently unknown) HVEW
 CC ligand, and to identify inhibitors of HSV-HVEW interaction.
 CC
 SQ Sequence 283 AA:


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XX 03-SEP-1999; 99WO-US20180.
PF
XX 03-SEP-1998; 98US-0146950.
PR 29-JUN-1999; 99US-0342767.
XX
XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX
XX Busfield ST;
XX
XX WPI: 2000-256981/22;
XX N-PSDB: AA294198.
XX
XX New nucleic acid molecule encoding herpes virus entry mediator (HVEM),
XX either in the soluble or membrane bound form, is useful in screening
XX assays and detection assays -
XX
XX Claim 8: Fig 7; 149pp; English.
XX
XX This polypeptide, the mature portion of which is also claimed,
XX is human membrane-bound herpesvirus entry mediator-2 (mHVEM2), a
XX novel form of membrane-bound herpesvirus entry mediator (mHVEM).
XX The amino acid sequence was deduced from an isolated cDNA clone
XX (see AA294198). mHVEM2 is a TANGO-69-receptor and member of the
XX tumour necrosis factor receptor (TNFR) superfamily. HVEM plays a
XX role in herpes simplex virus (HSV) entry. The invention is based
XX on the discovery of 3 cDNA molecules (see AA294195-97) which encode
XX soluble forms (see AA79204-06) of mHVEM, and the cDNA molecule
XX encoding of mHVEM2. In addition to isolated full-length proteins
XX and polynucleotides, and invention provides TANGO-69-receptor
XX fusion proteins, antigenic peptides and antibodies. Also provided
XX are recombinant expression vectors, host cells and transgenic
XX animals in which a TANGO-69-receptor gene has been introduced or
XX disrupted. DNA encoding HVEM, HVEM proteins and HVEM antibodies
XX can be used in screening and detection assays (e.g. chromosomal
XX mapping, tissue typing). HVEM proteins can also be used for
XX regulation of cell proliferation, cell differentiation, cell
XX survival, inflammation mast cell activity, HSV infection and/or
XX proliferation, and/or coagulation. HVEM agonists can be used to
XX treat disorders associated with decreased HVEM activity, e.g.
XX proliferative disorders such as carcinoma or pathogenic infection.
XX Antagonists can be used to treat disorders associated with
XX increased HVEM activity, e.g. autoimmune, T cell, inflammatory and
XX allergic inflammation disorders.
XX
XX Sequence 277 AA:
SQ

```

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Query Match      87.0%; Score 1373.5; DB 21; Length 277;
Best Local Similarity 93.5%; Pred. No. 2,1e-104;
Matches 245; Conservative 2; Mismatches 6; Indels 9; Gaps 1;

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    |||||||
DB 1 MEPPGWMGPPPRSTRPTVLRVLYLTLGAPCVAPALPSCKEEDYRPGSECCPCSG 60
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DB 61 YRKKEACGEITGVCPCPGTYIAHLNGISKLCOCMDPAMGLASRNCSTENAAG 120
    |||||||
OY 121 CSPGHECTIVQDDHCAACRAVATSSPGORVOKGTESDTLCONCPGTFSPNGTLECO 180
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DB 121 CSPGHECTIVQDDHCAACRAVATSSPGORVOKGTESDTLCONCPGTFSPNGTLECO 180
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    |||||||
DB 121 CSPGHECTIVQDDHCAACRAVATSSPGORVOKGTESDTLCONCPGTFSPNGTLECO 180
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OY 181 HQTGCMVLTAKGAGTSSSHWVWFLSGSLVIVYVSTYGLIICVARRKPRGDVAVIYS 240
    |||||||
DB 181 HQTGCMVLTAKGAGTSSSHWVWFLSGSLVIVYVSTYGLIICVARRKPRGDVAVIYS 240
    |||||||
OY 241 YORRRQEGAECAATFEALAPP 262
    |||||
DB 241 YORRRQEGAECAATFEALAPP 262
    |||||

```

```

RESULT 14
AA79204
ID AA79204 standard; Protein; 193 AA.
XX
XX AA79204;
XX
XX 19-JUN-2000 (first entry)
XX
XX Soluble herpesvirus entry mediator-1 (SHVEM1).
XX
XX SHVEM-1; soluble herpesvirus entry mediator-1; TANGO-69-receptor;
XX tumour necrosis factor receptor; human; herpes simplex virus;
XX infection; cancer; inflammation; autoimmune disorder; therapy;
XX diagnosis.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..36
XX /note= "signal peptide"
XX Protein 37..193
XX /note= "mature protein, also separately claimed
XX in Claim 8"
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XX Domain 42..75
XX /note= "cysteine-rich domain"
XX Domain 78..119
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XX Domain 121..162
XX /note= "cysteine-rich domain"
XX Modified-site 110
XX /note= "N-glycosylated"
XX Modified-site 173
XX /note= "N-glycosylated"
XX
XX WO200014230-A1.
XX
XX 16-MAR-2000.
XX
XX 03-SEP-1999; 99WO-US20180.
XX
XX 03-SEP-1998; 98US-0146950.
XX 29-JUN-1999; 99US-0342767.
XX
XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX
XX Busfield ST;
XX
XX WPI: 2000-256981/22.
XX N-PSDB: AA294195.
XX
XX New nucleic acid molecule encoding herpes virus entry mediator (HVEM),
XX either in the soluble or membrane bound form, is useful in screening
XX assays and detection assays -
XX
XX Claim 8: Fig 1; 149pp; English.
XX
XX This polypeptide, the mature portion of which is also claimed,
XX is human soluble herpesvirus entry mediator-1 (SHVEM1), a novel
XX soluble form of membrane-bound herpesvirus entry mediator (mHVEM).
XX The amino acid sequence was deduced from an isolated cDNA clone
XX (see AA294195). SHVEM1 is a TANGO-69-receptor and member of the
XX tumour necrosis factor receptor (TNFR) superfamily. It is
XX thought to play a role analogous to other soluble members of the
XX TNFR superfamily by interfering with the ability of LIGHT-TANGO-69
XX and lymphotoxin to bind mHVEM, and to play a role in herpes simplex
XX virus (HSV) entry. The invention is based on the discovery of 3
XX cDNA molecules (see AA294195-97) which encode soluble forms (see
XX AA79204-06), and 1 cDNA molecule (see AA294198) that encodes a 2nd
XX membrane-bound form (see AA79207), of mHVEM. In addition to
XX isolated full-length proteins and polynucleotides, and invention
XX provides TANGO-69-receptor fusion proteins, antigenic peptides and
XX antibodies. Also provided are recombinant expression vectors,
XX host cells and transgenic animals in which a TANGO-69-receptor

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Search completed: January 24, 2002, 16:21:43
Job time: 33 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 24, 2002, 16:21:10 ; Search time 12.68 seconds

(without alignments)
502.242 Million cell updates/sec

Title: US-08-741-095B-26

Perfect score: 1578

Sequence: 1 MEPPGDMGPPMRSTPRTDY.....VTVVAVEETIPFTGRSPNH 283

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: Issued_Patents_AA.*

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27: /cgn2_6/ptodata/2/1aa/6X_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1578	100.0	283	US-08-509-024-2	Sequence 2, Appli
2	1578	100.0	283	US-09-333-279-2	Sequence 2, Appli
3	1578	99.5	283	PCT-US96-12374-2	Sequence 2, Appli
4	1073	68.0	419	US-08-509-024-7	Sequence 7, Appli
5	1073	68.0	419	US-09-333-279-7	Sequence 7, Appli
6	1068	67.7	193	US-09-146-950-2	Sequence 2, Appli
7	1060	67.2	197	US-09-146-950-18	Sequence 2, Appli
8	847	53.7	155	US-09-146-950-4	Sequence 4, Appli
9	839	53.2	159	US-09-146-950-20	Sequence 20, Appli
10	365	23.1	77	US-09-146-950-25	Sequence 25, Appli
11	276.5	17.5	289	US-09-042-785A-11	Sequence 11, Appli
12	267.5	17.0	276	US-09-041-886-27	Sequence 27, Appli
13	267.5	17.0	277	US-09-042-785A-10	Sequence 10, Appli
14	267.5	17.0	277	US-09-006-353A-10	Sequence 10, Appli
15	260	16.5	207	US-08-974-022-47	Sequence 47, Appli
16	260	16.5	207	US-08-795-445A-47	Sequence 47, Appli
17	260	16.5	207	US-08-795-447A-47	Sequence 47, Appli
18	260	16.5	207	US-08-974-186-47	Sequence 47, Appli
19	260	16.5	207	US-08-795-446B-47	Sequence 47, Appli
20	260	16.5	325	US-08-292-549-2	Sequence 2, Appli
21	260	16.5	325	US-09-042-785A-9	Sequence 9, Appli
22	260	16.5	325	PCT-US91-02207-2	Sequence 2, Appli
23	259	16.4	445	US-09-146-950-9	Sequence 9, Appli
24	259	16.4	227	US-08-974-022-48	Sequence 48, Appli
25	259	16.4	227	US-08-795-445A-48	Sequence 48, Appli
26	259	16.4	227	US-08-795-447A-48	Sequence 48, Appli
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28	259	16.4	227	4	US-08-795-446B-48	Sequence 48, Appli
29	259	16.4	235	4	US-09-326-394-4	Sequence 4, Appli
30	259	16.4	461	1	US-08-385-229-2	Sequence 2, Appli
31	259	16.4	461	2	US-08-650-000-2	Sequence 2, Appli
32	259	16.4	461	4	US-09-042-785A-7	Sequence 7, Appli
33	259	16.4	461	4	US-08-477-347-3	Sequence 3, Appli
34	259	16.4	461	4	US-09-006-353A-4	Sequence 4, Appli
35	259	16.4	461	4	US-08-476-862-2	Sequence 2, Appli
36	259	16.4	461	6	5395760-2	Patent No. 5395760
37	259	16.4	486	1	US-08-243-010-1	Sequence 1, Appli
38	259	16.4	518	1	US-08-385-229-4	Sequence 4, Appli
39	258	16.3	197	3	US-08-974-022-49	Sequence 49, Appli
40	258	16.3	197	4	US-08-795-445A-49	Sequence 49, Appli
41	258	16.3	197	4	US-08-795-447A-49	Sequence 49, Appli
42	258	16.3	197	4	US-08-974-186-49	Sequence 49, Appli
43	258	16.3	197	4	US-08-795-446B-49	Sequence 49, Appli
44	257	16.3	162	2	US-08-219-237B-7	Sequence 7, Appli
45	257	16.3	162	4	US-08-476-862-7	Sequence 7, Appli

ALIGNMENTS

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RESULT 1
US-08-509-024-2
: Sequence 2, Application US/08509024B
: Patent No. 6291207
: GENERAL INFORMATION:
: APPLICANT: SPEAR, Patricia G.
: TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
: FILE REFERENCE: 0290-1
: CURRENT FILING DATE: 1995-07-25
: NUMBER OF SEQ ID NOS: 7
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 2
: LENGTH: 283
: TYPE: PRT
: ORGANISM: Homo sapiens
US-08-509-024-2

Query Match      100.0%; Score 1578; DB 4; Length 283;
Best Local Similarity 100.0%; Pred. No. 2.5e-134;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      181 HQTCKSMVLTVKAGAGTSSSHVWVFLSGSLVIVYVCSVGLIICVKKRRKPGDVVKVIVS 240
      |||

QY      241 VQRRKQEAEGEATVIEALQAPPDVYTVVAVEETIPFTGRSPNH 283
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DB      241 VQRRKQEAEGEATVIEALQAPPDVYTVVAVEETIPFTGRSPNH 283
      |||

RESULT 2
US-09-333-279-2
: Sequence 2, Application US/09333279
: Patent No. 630336
: GENERAL INFORMATION:
```



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RESULT 5
US-09-333-279-7
; Sequence 7, Application US/09333279
; Patent No. 630336
; GENERAL INFORMATION:
; APPLICANT: SPEAR, Patricia G.
; APPLICANT: MONTGOMERY, Rebecca I.
; TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
; FILE REFERENCE: 0290-1
; CURRENT APPLICATION NUMBER: US/09/333,279
; CURRENT FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-333-279-7
```

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Query Match          68.0%; Score 1073; DB 4; Length 419;
Best Local Similarity 100.0%; Pred. No. 9,5e-89;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 MEPPGDMGPPMWSPTPTDVLRLVLYLTFGLGAPCYAPALPSCKEDEXYPVGSCECCPKCSPG 60
DB 1 MEPPGDMGPPMWSPTPTDVLRLVLYLTFGLGAPCYAPALPSCKEDEXYPVGSCECCPKCSPG 60
QY 61 YRVEACGELGTGVCCEPCPGTYIAHLNGLSKLQCCMCDPAMGLASRNCSTENAVCG 120
DB 61 YRVEACGELGTGVCCEPCPGTYIAHLNGLSKLQCCMCDPAMGLASRNCSTENAVCG 120
QY 121 CSPGHFCIVDDGHCACRAVATSSPGQRYOKGSGTESQDILCONCPGTSPNGTLEECQ 180
DB 121 CSPGHFCIVDDGHCACRAVATSSPGQRYOKGSGTESQDILCONCPGTSPNGTLEECQ 180
QY 181 HQTKC 185
DB 181 HQTKC 185
```

```
RESULT 6
US-09-146-950-2
; Sequence 2, Application US/09146950A
; Patent No. 6287808
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
; FILE REFERENCE: 09404/057001
; CURRENT APPLICATION NUMBER: US/09/146,950A
; CURRENT FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-146-950-2
```

```
Query Match          67.7%; Score 1068; DB 4; Length 193;
Best Local Similarity 98.4%; Pred. No. 1e-88;
Matches 164; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 MEPPGDMGPPMWSPTPTDVLRLVLYLTFGLGAPCYAPALPSCKEDEXYPVGSCECCPKCSPG 60
DB 1 MEPPGDMGPPMWSPTPTDVLRLVLYLTFGLGAPCYAPALPSCKEDEXYPVGSCECCPKCSPG 60
QY 61 YRVEACGELGTGVCCEPCPGTYIAHLNGLSKLQCCMCDPAMGLASRNCSTENAVCG 120
DB 61 YRVEACGELGTGVCCEPCPGTYIAHLNGLSKLQCCMCDPAMGLASRNCSTENAVCG 120
```

```
QY 121 CSPGHFCIVDDGHCACRAVATSSPGQRYOKGSGTESQDILCONCPGTSPNGTLEECQ 180
DB 121 CSPGHFCIVDDGHCACRAVATSSPGQRYOKGSGTESQDILCONCPGTSPNGTLEECQ 180
QY 181 HQTKCSW 187
DB 181 HQTKCSW 187
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```
RESULT 7
US-09-146-950-18
; Sequence 18, Application US/09146950A
; Patent No. 6287808
```

```
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
; FILE REFERENCE: 09404/057001
; CURRENT APPLICATION NUMBER: US/09/146,950A
; CURRENT FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-146-950-18
```

```
Query Match          67.2%; Score 1060; DB 4; Length 197;
Best Local Similarity 98.4%; Pred. No. 5,6e-88;
Matches 184; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
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```
QY 1 MEPPGDMGPPMWSPTPTDVLRLVLYLTFGLGAPCYAPALPSCKEDEXYPVGSCECCPKCSPG 60
DB 1 MEPPGDMGPPMWSPTPTDVLRLVLYLTFGLGAPCYAPALPSCKEDEXYPVGSCECCPKCSPG 60
QY 61 YRVEACGELGTGVCCEPCPGTYIAHLNGLSKLQCCMCDPAMGLASRNCSTENAVCG 120
DB 61 YRVEACGELGTGVCCEPCPGTYIAHLNGLSKLQCCMCDPAMGLASRNCSTENAVCG 120
QY 121 CSPGHFCIVDDGHCACRAVATSSPGQRYOKGSGTESQDILCONCPGTSPNGTLEECQ 180
DB 121 CSPGHFCIVDDGHCACRAVATSSPGQRYOKGSGTESQDILCONCPGTSPNGTLEECQ 180
QY 181 HQTKCSW 187
DB 181 HQTKCSW 187
```

```
RESULT 8
US-09-146-950-4
; Sequence 4, Application US/09146950A
; Patent No. 6287808
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
; FILE REFERENCE: 09404/057001
; CURRENT APPLICATION NUMBER: US/09/146,950A
; CURRENT FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-146-950-4
```

```
Query Match          53.7%; Score 847; DB 4; Length 155;
Best Local Similarity 98.0%; Pred. No. 5,7e-69;
Matches 146; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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```

Oy      39  LPSCKEDEDEYVPGSECCPKCSPGYRVKKEACGELTGTVCPEPCPGTYIAHLNGLSKLQCCM 98
Db      1  LPSCKEDEYVPGSECCPKCSPGYRVKKEACGELTGTVCPEPCPGTYIAHLNGLSKLQCCM 60
Oy      99  CDPAMGLASRNSCRSTENAVAGCGSPGHFCIVQDDGHCACRAVATSSPGQVQKGTESQ 158
Db      61  CDPAMGLASRNSCRSTENAVAGCGSPGHFCIVQDDGHCACRAVATSSPGQVQKGTESQ 120
Oy      159 DTLQNCNCPRTFSPNGTLEECQHQTKCSW 187
Db      121 DTLQNCNCPRTFSPNGTLEECQHQTNAM 149

RESULT      9
US-09-146-950-20
; Sequence 20, Application US/09146950A
; Patent No. 6287808
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
; FILE REFERENCE: 09404/057001
; CURRENT APPLICATION NUMBER: US/09/146,950A
; CURRENT FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 159
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-146-950-20

```

```

Query Match Similarity      53.28; Score 839; DB 4; Length 159;
Best Local Similarity      98.0%; Pred. No. 3,1e-68;
Matches 146; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY      39  LPSCKEDDEYPVGSBCCPRKCSPGYRVRKEAGCELGTGVCPEPCPGTYIAHLNGLSKLQCOM 98
Db      1  LPSCKEDDEYPVGSBCCPRKCSPGYRVRKEAGCELGTGVCPEPCPGTYIAHLNGLSKLQCOM 60
QY      99  CDPAMGLPASNCRSTENAVGCGSPGHCTIVQDDHCAARAATSPGGRVKKGTETG 158
Db      61  CDPAMGLASNCRSTENAVGCGSPGHCTIVQDDHCAARAATSPGGRVKKGTETG 120
QY      159 DTLCONCPPTGTFSPNGTLEECOHQTKCS 187
Db      121 DTLCONCPPTGTFSPNGTLEECOHQTK--NW 147

RESULT 10
US-09-146-950-25
; Sequence 25, Application US/09146950A
; Patent No. 6287808
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 09404/057001
; CURRENT APPLICATION NUMBER: US/09/146,950A
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 77
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-146-950-25

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Query Match	23.1%;	Score 365;	DB 4;	Length 77;
Best Local Similarity	95.5%;	Pred. No. 4.9e-26;		

Matches	64; Conservative	1; Mismatches	0; Indels	2; Gaps	1;
OY	121	CSPGFCIVQDDHCAACRAVATSSPGQRYVQKGTSPDILCONCPGFSNGLTECQ		180	
Db	1	CSPGFCIVQDDHCAACRAVATSSPGQRYVQKGTSPDILCONCPGFSNGLTECQ		60	
OY	181	HOTKCSW	187		
Db	61	HQT--NW	65		

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	Query Match	17.5%	Score 276.5;	DB 4;	Length 289;
	Best Local Similarity	27.9%;	Pred. No. 2,2e-17;		
	Matches 69;	Conservative 43;	Mismatches 106;	Indels 29;	Gaps 8;
OY	41	SCRDEEDVVSBCCECKSPGYRVKAEAGELGTGVCEPCPCTGYIAHLNGLSKLQOCQMD	100		
Db	25	TCSDDXYLHDDCCDCLCPGSRILTSHTCALRKTCHPDSEFSXOMVREIRCHOHRICE	84		
OY	101	PAMGLRASRNCSTREANAYCGSPGHFCIVODGDHCACRAATSSPGOVRVGKGESDPT	160		
Db	85	PNQGRVKKEGTAEADVTCTCKEGHQHSKD---CEAQAQTPTCPIRGVEMMETETDT	141		
OY	161	LCQNPCTPEESPNGTL-BECHOHQTKS----WLYTKAGAGTSSSHIMWMFLSGSLVIYIV	215		
Db	142	VCHPEPVGEFESSNOSLFEKCYPMWSCDEBKNLEVLQK--GSQTNVICIGLKSRMRALVIYI	198		
OY	216	CSTVGLIIC-----VKK--RKPRGDVVKYIVSVQRROEAEEGATVIALQAPPDVYT	266		

Db 199 PYVNGILITIFGVETIKKVKKKKDN--EMLPPARQDPQME-----DYPGHNTA 249
QY 267 VAVEETI 273
Db 250 APVOETL 256

RESULT 12

US-09-041-886-27
Sequence 27, Application US/09041886
Patent No. 6235872
GENERAL INFORMATION:
APPLICANT: Bredesen, Dale E.
APPLICANT: Rabizadeh, Sharrooz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815,
REFERENCE/DOCKET NUMBER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 276 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-041-886-27

Query Match 17.0%; Score 267.5; DB 4; Length 276;
Best Local Similarity 26.1%; Pred. No. 1.3e-16;
Matches 71; Conservative 50; Mismatches 116; Indels 35; Gaps 9;

QY 20 VLRLVLYLFLGAPCYAPL-----PSCKEDXPVSGSECCPKSPGYRKEACGELTGY 74
Db 1 MYRLPLQCVLMG--CLLTAVHPEPTACREKQYLINSQCCSLQPOQKLVSDCTEFTETE 58
QY 75 CERCPEGTIVIAHLNGLSKLCQCOMCDPAMGLRASRNCSTRENAVCGSPGHFCIYODGDH 134
Db 59 CLPCGSEFLDYNRNRETHCHQHKYCDPNGLRYQOKGTSETDITICCEBGMHC---TSEA 115
QY 135 CAACRAVYATSSPGQRYQOKGTESQDTLCONCPGRTS--PNGTLEECOHOTKCSW--LVYK 191
Db 116 CESCVAHRCSPFGVKQIATGVSDTICEPCPYGFFSNVSSAFKCHPMTSCETKDLVYQ 175
QY 192 AGAGTSSHHMMWFLLSGSLVIVYVCGTGLIICVKKRRKRGDVVKYIVSYORRQAEGE 251
Db 176 Q-AGTKRTDVCGPDRRLALVVIPIIFGLFA-----ILLVLYFIKKVAKKPTNK 225
QY 252 ATVTEALQAPDV-----TTVAVEETI 273
Db 226 AP--HPKQEPQELNFPDDLPGSNTAPVQETL 255

RESULT 13

US-09-042-785A-10
Sequence 10, Application US/09042785A
Patent No. 6194151
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J
TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
TITLE OF INVENTION: AND USES THEREFOR
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESSES:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,785A
FILING DATE: 17-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/938,896
FILING DATE: 26-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: MEI-001CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-09-042-785A-10

Query Match 17.0%; Score 267.5; DB 4; Length 277;
Best Local Similarity 26.1%; Pred. No. 1.3e-16;
Matches 71; Conservative 50; Mismatches 116; Indels 35; Gaps 9;

QY 20 VLRLVLYLFLGAPCYAPL-----PSCKEDXPVSGSECCPKSPGYRKEACGELTGY 74
Db 1 MYRLPLQCVLMG--CLLTAVHPEPTACREKQYLINSQCCSLQPOQKLVSDCTEFTETE 58
QY 75 CERCPEGTIVIAHLNGLSKLCQCOMCDPAMGLRASRNCSTRENAVCGSPGHFCIYODGDH 134
Db 59 CLPCGSEFLDYNRNRETHCHQHKYCDPNGLRYQOKGTSETDITICCEBGMHC---TSEA 115
QY 135 CAACRAVYATSSPGQRYQOKGTESQDTLCONCPGRTS--PNGTLEECOHOTKCSW--LVYK 191
Db 116 CESCVAHRCSPFGVKQIATGVSDTICEPCPYGFFSNVSSAFKCHPMTSCETKDLVYQ 175
QY 192 AGAGTSSHHMMWFLLSGSLVIVYVCGTGLIICVKKRRKRGDVVKYIVSYORRQAEGE 251
Db 176 Q-AGTKRTDVCGPDRRLALVVIPIIFGLFA-----ILLVLYFIKKVAKKPTNK 225
QY 252 ATVTEALQAPDV-----TTVAVEETI 273
Db 226 AP--HPKQEPQELNFPDDLPGSNTAPVQETL 255
RESULT 14
US-09-006-353A-10
Sequence 10, Application US/09006353A

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/ Patent No. 6261801
/ GENERAL INFORMATION:
/ APPLICANT: WEI, YING-FEI
/ APPLICANT: YU, GUO-LIANG
/ APPLICANT: GENTZ, RETNER
/ APPLICANT: RUBEN, STEVEN
/ TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5
/ NUMBER OF SEQUENCES: 26
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: HUMAN GENOME SCIENCES, INC.
/ STREET: 9410 KEY WEST AVENUE
/ CITY: ROCKVILLE
/ STATE: MD
/ COUNTRY: US
/ ZIP: 20850
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/006,353A
/ FILING DATE:
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BROOKES, ANDERS A
/ REGISTRATION NUMBER: 36,373
/ REFERENCE/DOCKET NUMBER: PF341
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (301) 309-8504
/ TELEFAX: (301) 309-8512
/ INFORMATION FOR SEQ ID NO: 10:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 277 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-09-006-353A-10

Query Match 17.0%; Score 267.5; DB 4; Length 277;
Best Local Similarity 26.1%; Pred. No. 1.3e-16;
Matches 71; Conservative 50; Mismatches 116; Indels 35; Gaps 9;

OY 20 VLRVLVLYTLFLGAPCYAPAL-----PSCKDEYPVSECCPKSPGYRYKACGELGTG 74
DB 1 MVLRLPLQCVLMG--CLITAVHPEPPTRACREKQILINSQCCSLCPGOKLYSDCTEFETE 58
OY 75 CEECPPTGYIAHLNGLSKLQCCQCDPAMGLASRNCSTENAVCGSPGHFCIYODGDH 134
DB 59 CLPGCESEFLDTWNRRETHCHQHKYCDPNLGLRVQKGTSETDITCTCEEGMHC---TSEA 115
OY 135 CAACRAVATSSPGQRYOKGTESDPTLCQNCPPGTFS--PGTLECOHQKCSM--LYTK 191
DB 116 CESCVLHRSQSPGFGVKQIATGVSDTCEPCPVGFNSVSAFEKCPHWTSCETKDLVQ 175
OY 192 AGAGTSSSHVMWFLSGSLIVIVICSTVGLICVKKRRKPGDVKVYVSRKROEAEGE 251
DB 176 Q-AGTKTIDVYCGPDRRLRLALVYIPIIFGILFA-----ILLVYVFIKKYAKKPTNK 225
OY 252 ATVIEALQAPPDY-----TTVAVEETI 273
DB 226 AP--HPKQEPQIINFDDLPGSNTAAVQETL 255
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RESULT 15
US-08-974-022-47
Sequence 47, Application US/08974022
Patent No. 6015938

GENERAL INFORMATION:
APPLICANT: Boyle, William J.
APPLICANT: Lacey, David L.

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/ APPLICANT: Calzone, Frank J.
/ APPLICANT: Chang, Ming-Shi
/ TITLE OF INVENTION: OSTEOPROTEGERIN
/ NUMBER OF SEQUENCES: 53
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Amgen Inc.
/ STREET: 1840 Dehavilland Drive
/ CITY: Thousand Oaks
/ STATE: California
/ COUNTRY: USA
/ ZIP: 91320-1789
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/974,022
/ FILING DATE: 12-DEC-1995
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/577,788
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Winter, Robert B.
/ REFERENCE/DOCKET NUMBER: A-378
/ INFORMATION FOR SEQ ID NO: 47:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 207 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-974-022-47

Query Match 16.5%; Score 260; DB 3; Length 207;
Best Local Similarity 31.5%; Pred. No. 4.4e-16;
Matches 62; Conservative 25; Mismatches 80; Indels 30; Gaps 8;

OY 20 VLRVLVLYTLFLGAPCYAPAL-----SCKDEYPVSECCPKSPGYRYKACGELGTG 73
DB 1 MRLRLALVGV--VYVGDVDPYSSNOGCGHDEKDLCCASCSPGFVYASRLCGPSMT 59
OY 74 VCECPPTGYIAHLNGLSKLQCCQCDPAMG-LRASRNCSTENAVCGSPGHFCIYODG 132
DB 60 VCSCEEGTFTASTNHAPACVSCR--GPTGHLSESGPCDRTHRYVNCSTGNCLLKQ 117
OY 133 DHCACRAVATSSPGQRYOKGTESDPTLCQNCPPGTFSN--GTLEEC----- 179
DB 118 NGCRIC-APQTKCPAGYGVSCHTRAGDILCEKCPHTYSDSLPTERCSTSFNYISVGFN 176
OY 180 ---QHOKCSMLVYTKAG 193
DB 177 LYPVNETSCT---TTAG 190
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Search completed: January 24, 2002, 16:22:02
Job time: 52 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 24, 2002, 16:21:15 ; Search time 97.61 Seconds
(without alignments)
805.009 Million cell updates/sec

Title: US-08-741-095b-26
Perfect score: 1578
Sequence: 1 MEPPCDWGPMPRSTPRDY.....VTVAVEETIPFTGRSPNH 283

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3148936 seqs, 277657034 residues
Total number of hits satisfying chosen parameters: 3148936

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Pending_Patents_AA_Main:*

- 1: /cgn2_6/ptodata/2/paa/PCRTUS_COMB.pep.*
- 2: /cgn2_6/ptodata/2/paa/US06_COMB.pep.*
- 3: /cgn2_6/ptodata/2/paa/US07_COMB.pep.*
- 4: /cgn2_6/ptodata/2/paa/US08_COMB.pep.*
- 5: /cgn2_6/ptodata/2/paa/US081_COMB.pep.*
- 6: /cgn2_6/ptodata/2/paa/US082_COMB.pep.*
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- 23: /cgn2_6/ptodata/2/paa/US099_COMB.pep.*
- 24: /cgn2_6/ptodata/2/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1578	100.0	283	1	PCT-US01-26396-31
2	1578	100.0	283	1	PCT-US95-05058-2
3	1578	100.0	283	1	PCT-US99-20180-13
4	1578	100.0	283	8	US-08-462-315-2
5	1578	100.0	283	8	US-08-462-962-2
6	1578	100.0	283	8	US-08-464-585-2
7	1578	100.0	283	11	US-08-741-095b-26
8	1578	100.0	283	13	US-08-987-902-1
9	1578	100.0	283	17	US-09-342-767-13

10	1578	100.0	283	18	US-09-480-284-1	Sequence 1, Appli
11	1578	100.0	283	19	US-09-533-262-26	Sequence 26, Appl
12	1578	100.0	283	22	US-09-882-636-46	Sequence 46, Appl
13	1578	100.0	283	22	US-09-886-342-60	Sequence 60, Appl
14	1578	100.0	283	23	US-09-935-727-31	Sequence 31, Appl
15	1575	99.8	283	1	PCT-US96-18540-2	Sequence 2, Appli
16	1575	99.8	283	11	US-08-741-095a-2	Sequence 2, Appli
17	1575	99.8	283	11	US-08-741-095a-2	Sequence 2, Appli
18	1575	99.8	283	11	US-08-741-095a-2	Sequence 26, Appl
19	1575	99.8	283	11	US-08-741-095b-26	Sequence 26, Appl
20	1575	99.8	283	17	US-09-340-690-2	Sequence 2, Appli
21	1575	99.8	283	17	US-09-340-690-26	Sequence 26, Appl
22	1575	99.8	283	18	US-09-403-815-2	Sequence 2, Appli
23	1575	99.8	283	19	US-09-533-262-2	Sequence 2, Appli
24	1575	99.8	283	24	US-60-125-683-2	Sequence 2, Appli
25	1575	99.8	283	24	US-60-135-169-2	Sequence 2, Appli
26	1575	99.8	284	21	US-09-760-455-73	Sequence 73, Appl
27	1575	99.8	284	21	US-09-760-485-874	Sequence 874, App
28	1572	99.6	283	14	US-09-072-993-2	Sequence 2, Appli
29	1572	99.6	283	14	US-09-072-993C-2	Sequence 2, Appli
30	1572	99.6	283	14	US-09-072-993B-2	Sequence 2, Appli
31	1572	99.6	655	14	US-08-072-993B-2	Sequence 2, Appli
32	1570	99.5	283	13	US-08-955-531-4	Sequence 4, Appli
33	1373.5	87.0	277	1	PCT-US99-20180-42	Sequence 42, Appl
34	1373.5	87.0	277	1	US-09-342-767-42	Sequence 42, Appl
35	1152.5	73.0	239	1	PCT-US99-20180-44	Sequence 44, Appl
36	1152.5	73.0	239	17	US-09-342-767-44	Sequence 44, Appl
37	1068	67.7	193	1	PCT-US99-20180-2	Sequence 2, Appli
38	1068	67.7	193	17	US-09-342-767-2	Sequence 2, Appli
39	1060	67.2	197	1	PCT-US99-20180-18	Sequence 18, Appl
40	1060	67.2	197	17	US-09-342-767-18	Sequence 18, Appl
41	1058	67.0	186	1	PCT-US99-20180-30	Sequence 30, Appl
42	1058	67.0	186	17	US-09-342-767-30	Sequence 30, Appl
43	908.5	57.6	161	19	US-09-523-323-56	Sequence 56, Appl
44	908.5	57.6	161	24	US-60-137-457-56	Sequence 56, Appl
45	908.5	57.6	161	24	US-60-142-657-56	Sequence 56, Appl

ALIGNMENTS

RESULT 1
PCT-US01-26396-31
Sequence 31, Application PC/RTUS0126396
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
FILE REFERENCE: PF454PCT3
CURRENT APPLICATION NUMBER: PCT/US01/26396
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/303,224
PRIOR FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: 60/252,131
PRIOR FILING DATE: 2000-11-21
PRIOR APPLICATION NUMBER: 60/227,598
PRIOR FILING DATE: 2000-08-25
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 31
LENGTH: 283
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US01-26396-31

Query Match 100.0%; Score 1578; DB 1; Length 283;
Best Local Similarity 100.0%; Pred. No. 3.6e-119;
Matches 283; Conservative 0; Mismatches 0; Indels. 0; Gaps 0;
OY 1 MEPPCDWGPMPRSTPRDYLVLTFLGAPCYAPALPSCKEDEYVGSCECPKCSFG 60
DB 1 MEPPCDWGPMPRSTPRDYLVLTFLGAPCYAPALPSCKEDEYVGSCECPKCSFG 60

QY 61 YRVKACGELTGVCEPCPGTYIAHLNGLSKLQCMCDPAMGLRASRNCSTENAVCG 120
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Db 61 YRVKACGELTGVCEPCPGTYIAHLNGLSKLQCMCDPAMGLRASRNCSTENAVCG 120
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QY 121 CSPGHFCIVODGDHCAACRAVATSSPGQROVKGSTESODTLQCNCPGTFSPNCTLEECQ 180
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Db 121 CSPGHFCIVODGDHCAACRAVATSSPGQROVKGSTESODTLQCNCPGTFSPNCTLEECQ 180
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QY 181 HQTKCSMLVTRKAGAGTSSSHWMMFLSGSLVIYIVCSTVGLITCVKRRKRGDVVKYIVS 240
| | | | |
Db 181 HQTKCSMLVTRKAGAGTSSSHWMMFLSGSLVIYIVCSTVGLITCVKRRKRGDVVKYIVS 240
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QY 241 VORRQBAEGEATVIEALQAPPDVTVAVEETIPSTGSRPNH 283
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Db 241 VORRQBAEGEATVIEALQAPPDVTVAVEETIPSTGSRPNH 283
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RESULT 2
PCT-US95-05058-2
; Sequence 2, Application PC/TUS9505058
; GENERAL INFORMATION:
; APPLICANT: NI, ET AL.
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARBELL, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05058
; FILING DATE: Concurrently
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-255
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ. ID NO. 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 283 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; PCT-US95-05058-2

Query Match 100.0%; Score 1578; DB 1; Length 283;
Best Local Similarity 100.0%; Pred. No. 3,6e-119;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MEPPGDMGPPPMSTPRTDVLRLVLYLTFGLGAPCYAPALPSCKEDEXPVGSECCPKCSPG 60
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QY 61 YRVKACGELTGVCEPCPGTYIAHLNGLSKLQCMCDPAMGLRASRNCSTENAVCG 120
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Db 121 CSPGHFCIVODGDHCAACRAVATSSPGQROVKGSTESODTLQCNCPGTFSPNCTLEECQ 180
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QY 181 HQTKCSMLVTRKAGAGTSSSHWMMFLSGSLVIYIVCSTVGLITCVKRRKRGDVVKYIVS 240
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QY 241 VORRQBAEGEATVIEALQAPPDVTVAVEETIPSTGSRPNH 283
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RESULT 3
PCT-US99-20180-13
; Sequence 13, Application PC/TUS9920180
; GENERAL INFORMATION:
; APPLICANT: Millennium Biotherapeutics, Inc.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HERPESVIRUS-ENTRY-MEDIATOR-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: 09404/079W01
; CURRENT APPLICATION NUMBER: PCT/US99/20180
; CURRENT FILING DATE: 1999-09-03
; EARLIER APPLICATION NUMBER: US 09/342,767
; EARLIER FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: US 09/146,950
; EARLIER FILING DATE: 1998-09-03
; NUMBER OF SEQ. ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ. ID NO. 13
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(38)
; PCT-US99-20180-13

Query Match 100.0%; Score 1578; DB 1; Length 283;
Best Local Similarity 100.0%; Pred. No. 3,6e-119;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPPMSTPRTDVLRLVLYLTFGLGAPCYAPALPSCKEDEXPVGSECCPKCSPG 60
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Db 1 MEPPGDMGPPPMSTPRTDVLRLVLYLTFGLGAPCYAPALPSCKEDEXPVGSECCPKCSPG 60
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QY 61 YRVKACGELTGVCEPCPGTYIAHLNGLSKLQCMCDPAMGLRASRNCSTENAVCG 120
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Db 61 YRVKACGELTGVCEPCPGTYIAHLNGLSKLQCMCDPAMGLRASRNCSTENAVCG 120
| | | | |
QY 121 CSPGHFCIVODGDHCAACRAVATSSPGQROVKGSTESODTLQCNCPGTFSPNCTLEECQ 180
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QY 181 HQTKCSMLVTRKAGAGTSSSHWMMFLSGSLVIYIVCSTVGLITCVKRRKRGDVVKYIVS 240
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Db 181 HQTKCSMLVTRKAGAGTSSSHWMMFLSGSLVIYIVCSTVGLITCVKRRKRGDVVKYIVS 240
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Db 241 VORRQBAEGEATVIEALQAPPDVTVAVEETIPSTGSRPNH 283
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RESULT 4
US-08-462-315-2
; Sequence 2, Application US/08462315
; GENERAL INFORMATION:
; APPLICANT: NI, ET AL.
; TITLE OF INVENTION: Tumor Necrosis Factor Receptors
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARBELL, BYRNE, BAIN, GILFILLAN,

ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462.315
FILING DATE: June 5, 1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05058
FILING DATE: 27 APR 95
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-421
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 283 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-462-315-2

Query Match 100.0%; Score 1578; DB 8; Length 283;
Best Local Similarity 100.0%; Pred. No. 3.6e-119;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 YRVKACGELTGTVEPCPGTYIAHLNGLSKLCQCMCDPMGIRASRNCRTENAVCG 120
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DB 121 CSPGHFCIVODGDHCAACRAVATSSPGQVOKGTESDTLQNCPPGTFSPNGTLEECQ 180
QY 181 HOTKCSMLVTAGAGTSSSHWWMFLSGSLVIVICSTVGLIICVKKRRPRGDVYKVIYS 240
DB 181 HOTKCSMLVTAGAGTSSSHWWMFLSGSLVIVICSTVGLIICVKKRRPRGDVYKVIYS 240
QY 241 VQKRQEAEGEATVIEALQAPPDVTVAVEETIPSTGRSPNH 283
DB 241 VQKRQEAEGEATVIEALQAPPDVTVAVEETIPSTGRSPNH 283

RESULT 5
US-08-462-962-2
Sequence 2, Application US/08462962
GENERAL INFORMATION:
APPLICANT: NI, ET AL.
TITLE OF INVENTION: Tumor Necrosis Factor Receptors
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY

COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462.962
FILING DATE: June 5, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05058
FILING DATE: 27 APR 95
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-422
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 283 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-462-962-2

Query Match 100.0%; Score 1578; DB 8; Length 283;
Best Local Similarity 100.0%; Pred. No. 3.6e-119;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPPGDMGPPPRSRPRDVLRLVLYLFLGAPCYAPALPSCKEDEYVGSCECPKCSPG 60
DB 1 MPPGDMGPPPRSRPRDVLRLVLYLFLGAPCYAPALPSCKEDEYVGSCECPKCSPG 60
QY 61 YRVKACGELTGTVEPCPGTYIAHLNGLSKLCQCMCDPMGIRASRNCRTENAVCG 120
DB 61 YRVKACGELTGTVEPCPGTYIAHLNGLSKLCQCMCDPMGIRASRNCRTENAVCG 120
QY 121 CSPGHFCIVODGDHCAACRAVATSSPGQVOKGTESDTLQNCPPGTFSPNGTLEECQ 180
DB 121 CSPGHFCIVODGDHCAACRAVATSSPGQVOKGTESDTLQNCPPGTFSPNGTLEECQ 180
QY 181 HOTKCSMLVTAGAGTSSSHWWMFLSGSLVIVICSTVGLIICVKKRRPRGDVYKVIYS 240
DB 181 HOTKCSMLVTAGAGTSSSHWWMFLSGSLVIVICSTVGLIICVKKRRPRGDVYKVIYS 240
QY 241 VQKRQEAEGEATVIEALQAPPDVTVAVEETIPSTGRSPNH 283
DB 241 VQKRQEAEGEATVIEALQAPPDVTVAVEETIPSTGRSPNH 283

RESULT 6
US-08-464-595-2
Sequence 2, Application US/08464595
GENERAL INFORMATION:
APPLICANT: JIAN NI, REINER GENTZ AND CRAIG ROSEN
TITLE OF INVENTION: Tumor Necrosis Factor Receptors
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE

COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,595
FILING DATE: June 5, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05058
FILING DATE: April 27, 1995
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-375
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 283 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-464-595-2

Query Match 100.0%; Score 1578; DB 8; Length 283;
Best Local Similarity 100.0%; Pred. No. 3.6e-119;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGMGPPPMRSTPRTDVLRLVLTFLGAPCYAPALPSCKEDEYVPGSECCPKCSPG 60
DB 1 MEPPGMGPPPMRSTPRTDVLRLVLTFLGAPCYAPALPSCKEDEYVPGSECCPKCSPG 60
QY 61 YRKACGELGTGVCPCPGTYIAHLNGLSKLQCMCPANGLRASRNCSTENAVCG 120
DB 61 YRKACGELGTGVCPCPGTYIAHLNGLSKLQCMCPANGLRASRNCSTENAVCG 120
QY 121 CSPGHFCIVODGDHCAACRAVATSSPGQRYQKGTESODTLQNCPCPGTSPNGTLEECQ 180
DB 121 CSPGHFCIVODGDHCAACRAVATSSPGQRYQKGTESODTLQNCPCPGTSPNGTLEECQ 180
QY 181 HOTKCSMLYTKAGAGTSSSHWMMFLSGSLVIYVCSVGLIICVRRKRGDVAVYIS 240
DB 181 HOTKCSMLYTKAGAGTSSSHWMMFLSGSLVIYVCSVGLIICVRRKRGDVAVYIS 240
QY 241 YQRRQAEAGEATVIEALQAPPDVTVAVEETIPSTGRSPNH 283
DB 241 YQRRQAEAGEATVIEALQAPPDVTVAVEETIPSTGRSPNH 283

RESULT 7
US-08-741-095b-26
Sequence 26, Application US/08741095B
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Rosen, Craig
APPLICANT: Genetz, Reiner
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like 2
FILE REFERENCE: 1488, 0770004
CURRENT APPLICATION NUMBER: US/08/741,095B
CURRENT FILING DATE: 1996-10-30
PRIOR APPLICATION NUMBER: US 08/464,595
PRIOR FILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: US 08/462,962
PRIOR FILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: US 08/462,315
PRIOR FILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: PCT/US95/05058
PRIOR FILING DATE: 1995-04-27
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PatentIn version 3.0

SEQ ID NO 26
LENGTH: 283
TYPE: PRT
ORGANISM: Homo sapiens
US-08-741-095b-26

Query Match 100.0%; Score 1578; DB 11; Length 283;
Best Local Similarity 100.0%; Pred. No. 3.6e-119;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGMGPPPMRSTPRTDVLRLVLTFLGAPCYAPALPSCKEDEYVPGSECCPKCSPG 60
DB 1 MEPPGMGPPPMRSTPRTDVLRLVLTFLGAPCYAPALPSCKEDEYVPGSECCPKCSPG 60
QY 61 YRKACGELGTGVCPCPGTYIAHLNGLSKLQCMCPANGLRASRNCSTENAVCG 120
DB 61 YRKACGELGTGVCPCPGTYIAHLNGLSKLQCMCPANGLRASRNCSTENAVCG 120
QY 121 CSPGHFCIVODGDHCAACRAVATSSPGQRYQKGTESODTLQNCPCPGTSPNGTLEECQ 180
DB 121 CSPGHFCIVODGDHCAACRAVATSSPGQRYQKGTESODTLQNCPCPGTSPNGTLEECQ 180
QY 181 HOTKCSMLYTKAGAGTSSSHWMMFLSGSLVIYVCSVGLIICVRRKRGDVAVYIS 240
DB 181 HOTKCSMLYTKAGAGTSSSHWMMFLSGSLVIYVCSVGLIICVRRKRGDVAVYIS 240
QY 241 YQRRQAEAGEATVIEALQAPPDVTVAVEETIPSTGRSPNH 283
DB 241 YQRRQAEAGEATVIEALQAPPDVTVAVEETIPSTGRSPNH 283

RESULT 8
US-08-987-902-1

Sequence 1, Application US/08987902
GENERAL INFORMATION:
APPLICANT: Avi J. Ashkenazi and Scot A. Marsters
TITLE OF INVENTION: HVEM Polypeptides and Uses Thereof
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/987,902
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1068R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 283 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-987-902-1

Query Match 100.0%; Score 1578; DB 13; Length 283;
Best Local Similarity 100.0%; Pred. No. 3.6e-119;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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QY 1 MEPPGDMGPPMRSTPRTDVLRLVLYLTLFLGAPCYAPALPSCKEDEYPVGSECCPCSPG 60
;
;
;
Db 1 MEPPGDMGPPMRSTPRTDVLRLVLYLTLFLGAPCYAPALPSCKEDEYPVGSECCPCSPG 60
;
;
;
QY 61 YRKEACGELTGTVCPCPGTYIAHLNGLSKLOCQOMCDPAMGLRASRNCSTENAVCG 120
;
;
;
Db 61 YRKEACGELTGTVCPCPGTYIAHLNGLSKLOCQOMCDPAMGLRASRNCSTENAVCG 120
;
;
;
QY 121 CSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESODTLQONCPPTGTFSPNGTLEEQ 180
;
;
;
Db 121 CSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESODTLQONCPPTGTFSPNGTLEEQ 180
;
;
;
QY 181 HOTKCSMLVTKAGAGTSSSHWMMFLSGSLVYIVCSTYGLIICVRRKPRGDDVAVYIS 240
;
;
;
Db 181 HOTKCSMLVTKAGAGTSSSHWMMFLSGSLVYIVCSTYGLIICVRRKPRGDDVAVYIS 240
;
;
;
QY 241 VORRROEAGEATVIEALQAPPDVTTVAEETIPSTGSPNH 283
;
;
;
Db 241 VORRROEAGEATVIEALQAPPDVTTVAEETIPSTGSPNH 283
;
;
;

```

RESULT 9

```

US-09-342-767-13
; Sequence 13, Application US/09342767
;
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE
; TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: MBI098-06ICPI
; CURRENT APPLICATION NUMBER: US/09/342,767
; EARLIER FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: US 09/146,950
; EARLIER FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(38)
US-09-342-767-13

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Query Match 100.0%; Score 1578; DB 17; Length 283;

Best Local Similarity 100.0%; Pred. No. 3.6e-119;

Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MEPPGDMGPPMRSTPRTDVLRLVLYLTLFLGAPCYAPALPSCKEDEYPVGSECCPCSPG 60
;
;
;
Db 1 MEPPGDMGPPMRSTPRTDVLRLVLYLTLFLGAPCYAPALPSCKEDEYPVGSECCPCSPG 60
;
;
;
QY 61 YRKEACGELTGTVCPCPGTYIAHLNGLSKLOCQOMCDPAMGLRASRNCSTENAVCG 120
;
;
;
Db 61 YRKEACGELTGTVCPCPGTYIAHLNGLSKLOCQOMCDPAMGLRASRNCSTENAVCG 120
;
;
;
QY 121 CSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESODTLQONCPPTGTFSPNGTLEEQ 180
;
;
;
Db 121 CSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESODTLQONCPPTGTFSPNGTLEEQ 180
;
;
;
QY 181 HOTKCSMLVTKAGAGTSSSHWMMFLSGSLVYIVCSTYGLIICVRRKPRGDDVAVYIS 240
;
;
;
Db 181 HOTKCSMLVTKAGAGTSSSHWMMFLSGSLVYIVCSTYGLIICVRRKPRGDDVAVYIS 240
;
;
;
QY 241 VORRROEAGEATVIEALQAPPDVTTVAEETIPSTGSPNH 283
;
;
;
Db 241 VORRROEAGEATVIEALQAPPDVTTVAEETIPSTGSPNH 283
;
;
;

```

RESULT 10

```

US-09-480-284-1
; Sequence 1, Application US/09480284
;
; GENERAL INFORMATION:
; APPLICANT: Avi J. Ashkenazi and Scot A. Marsters
; TITLE OF INVENTION: HIVM Polypeptides and Uses Thereof
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/480,284
; FILING DATE: 10-Jan-2000
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/987,902
; FILING DATE: 10-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1068R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
;
; INFORMATION FOR SEQ ID NO: 1:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 283 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-480-284-1

```

Query Match 100.0%; Score 1578; DB 18; Length 283;

Best Local Similarity 100.0%; Pred. No. 3.6e-119;

Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MEPPGDMGPPMRSTPRTDVLRLVLYLTLFLGAPCYAPALPSCKEDEYPVGSECCPCSPG 60
;
;
;
Db 1 MEPPGDMGPPMRSTPRTDVLRLVLYLTLFLGAPCYAPALPSCKEDEYPVGSECCPCSPG 60
;
;
;
QY 61 YRKEACGELTGTVCPCPGTYIAHLNGLSKLOCQOMCDPAMGLRASRNCSTENAVCG 120
;
;
;
Db 61 YRKEACGELTGTVCPCPGTYIAHLNGLSKLOCQOMCDPAMGLRASRNCSTENAVCG 120
;
;
;
QY 121 CSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESODTLQONCPPTGTFSPNGTLEEQ 180
;
;
;
Db 121 CSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESODTLQONCPPTGTFSPNGTLEEQ 180
;
;
;
QY 181 HOTKCSMLVTKAGAGTSSSHWMMFLSGSLVYIVCSTYGLIICVRRKPRGDDVAVYIS 240
;
;
;
Db 181 HOTKCSMLVTKAGAGTSSSHWMMFLSGSLVYIVCSTYGLIICVRRKPRGDDVAVYIS 240
;
;
;
QY 241 VORRROEAGEATVIEALQAPPDVTTVAEETIPSTGSPNH 283
;
;
;
Db 241 VORRROEAGEATVIEALQAPPDVTTVAEETIPSTGSPNH 283
;
;
;

```

RESULT 11

```

US-09-533-262-26
; Sequence 26, Application US/09533262
;
; GENERAL INFORMATION:
; APPLICANT: NI, Jian
; APPLICANT: Rosen, Craig A.
; APPLICANT: Gentz, Reiner L.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like 2

```

FILE REFERENCE: 1488.077000A
CURRENT APPLICATION NUMBER: US/09/533,262
EARLIER FILING DATE: 2000-03-22
EARLIER APPLICATION NUMBER: US 60/147,383
EARLIER FILING DATE: 1999-08-06
EARLIER APPLICATION NUMBER: US 60/135,169
EARLIER FILING DATE: 1999-05-20
EARLIER APPLICATION NUMBER: US 60/126,522
EARLIER FILING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: US 60/125,683
EARLIER FILING DATE: 1999-03-22
EARLIER APPLICATION NUMBER: US 08/741,095
EARLIER FILING DATE: 1996-10-30
EARLIER APPLICATION NUMBER: US 08/464,595
EARLIER FILING DATE: 1995-06-05
EARLIER APPLICATION NUMBER: US 08/462,962
EARLIER FILING DATE: 1995-06-05
EARLIER APPLICATION NUMBER: US 08/462,315
EARLIER FILING DATE: 1995-06-05
EARLIER APPLICATION NUMBER: PCT/US95/05058
EARLIER FILING DATE: 1995-04-27
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.0
SEO ID NO: 26
LENGTH: 283
TYPE: PRT
ORGANISM: Homo sapiens
US-09-533-262-26

Query Match 100.0%; Score 1578; DB 19; Length 283;
Best Local Similarity 100.0%; Pred. No. 3.6e-119;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGWMGPPWRSTPRTDVLRLVLTETGACQVAPALPSCKEDEYVPGSECCPKCSPG 60
DB 1 MEPPGWMGPPWRSTPRTDVLRLVLTETGACQVAPALPSCKEDEYVPGSECCPKCSPG 60
QY 61 YRKEACGELTGVCEPCPGTIAHNGSKLQCOMCPANGLRASRNCSTENAVCG 120
DB 61 YRKEACGELTGVCEPCPGTIAHNGSKLQCOMCPANGLRASRNCSTENAVCG 120
QY 121 CSPGHCIVODGDHCAACRAVATSPGQRYQKGTESQDTLQNCPEGTFSPNGTLEECQ 180
DB 121 CSPGHCIVODGDHCAACRAVATSPGQRYQKGTESQDTLQNCPEGTFSPNGTLEECQ 180
QY 181 HQKCSMLTKAGAGTSSSHWMMFISGSLVIVYVCSVGLIICVKKRKRGRGVKVIYS 240
DB 181 HQKCSMLTKAGAGTSSSHWMMFISGSLVIVYVCSVGLIICVKKRKRGRGVKVIYS 240
QY 241 VOKRQAEAEATVIALQAPDVTVAVEETIPSTGSRPNH 283
DB 241 VOKRQAEAEATVIALQAPDVTVAVEETIPSTGSRPNH 283

RESULT 12
US-09-882-636-46
Sequence 46, Application US/09882636
GENERAL INFORMATION:
APPLICANT: Botstein, David
APPLICANT: Goddard, Audrey
APPLICANT: Gurley, Austin L.
APPLICANT: Hillan, Kenneth
APPLICANT: Lawrence, David, A
APPLICANT: Roy, Margaret, Ann
APPLICANT: Wood, William, I.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR
FILE REFERENCE: P2509R1C1
CURRENT APPLICATION NUMBER: US/09/882,636
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/112,850

PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/107,783
PRIOR FILING DATE: November 10, 1998
PRIOR APPLICATION NUMBER: 60/088,742
PRIOR FILING DATE: June 10, 1998
PRIOR APPLICATION NUMBER: 60/086,414
PRIOR FILING DATE: May 22, 1998
PRIOR APPLICATION NUMBER: 60/083,500
PRIOR FILING DATE: April 29, 1998
PRIOR APPLICATION NUMBER: 60/082,767
PRIOR FILING DATE: April 23, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/066,772
PRIOR FILING DATE: November 24, 1997
PRIOR APPLICATION NUMBER: 60/032,705
PRIOR FILING DATE: December 12, 1996
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: 09/709,238
PRIOR FILING DATE: November 8, 2000
PRIOR APPLICATION NUMBER: 09/664,610
PRIOR FILING DATE: September 18, 2000
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: September 18, 2000
PRIOR APPLICATION NUMBER: PCT/US00/23522
PRIOR FILING DATE: August 23, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14941
PRIOR FILING DATE: May 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/13705
PRIOR FILING DATE: May 17, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05004
PRIOR FILING DATE: February 24, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04341
PRIOR FILING DATE: February 18, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04342
PRIOR FILING DATE: February 18, 2000
PRIOR APPLICATION NUMBER: 09/480,284
PRIOR FILING DATE: January 10, 2000
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: December 2, 1999
PRIOR APPLICATION NUMBER: 09/423,844
PRIOR FILING DATE: November 12, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: November 30, 1999
PRIOR APPLICATION NUMBER: 09/403,297
PRIOR FILING DATE: October 18, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/20111
PRIOR FILING DATE: September 1, 1999
PRIOR APPLICATION NUMBER: 09/380,137
PRIOR FILING DATE: August 25, 1999

;; PRIOR APPLICATION NUMBER: 09/380,138
;; PRIOR FILING DATE: August 25, 1999
;; PRIOR APPLICATION NUMBER: 09/380,139
;; PRIOR FILING DATE: August 25, 1999
;; PRIOR APPLICATION NUMBER: 09/367,206
;; PRIOR FILING DATE: August 9, 1999
;; PRIOR APPLICATION NUMBER: 09/369,028
;; PRIOR FILING DATE: August 4, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: June 2, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/08847
;; PRIOR FILING DATE: April 23, 1999
;; PRIOR APPLICATION NUMBER: 09/298,404
;; PRIOR FILING DATE: April 23, 1999
;; PRIOR APPLICATION NUMBER: 09/284,291
;; PRIOR FILING DATE: April 12, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/05028
;; PRIOR FILING DATE: March 8, 1999
;; PRIOR APPLICATION NUMBER: 09/254,311
;; PRIOR FILING DATE: March 3, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/00106
;; PRIOR FILING DATE: January 5, 1999
;; PRIOR APPLICATION NUMBER: 09/218,517
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 09/216,021
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: PCT/US98/25108
;; PRIOR FILING DATE: December 1, 1998
;; PRIOR APPLICATION NUMBER: PCT/US98/19330
;; PRIOR FILING DATE: September 16, 1998
;; PRIOR APPLICATION NUMBER: 09/065,275
;; PRIOR FILING DATE: April 23, 1998
;; PRIOR APPLICATION NUMBER: 08/987,902
;; PRIOR FILING DATE: December 10, 1997
;; PRIOR APPLICATION NUMBER: PCT/US97/22278
;; PRIOR FILING DATE: December 5, 1997
;; NUMBER OF SEQ ID NOS: 113
;; SEQ ID NO: 46
;; LENGTH: 283
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-882-636-46

Query Match 100.0%; Score 1578; DB 22; Length 283;
Best Local Similarity 100.0%; Pred. No. 3.6e-119;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPPGDMGPPPRSTPRDVLRLVLYLTFELGAPCYAPALPSCKEDEYPVGSCCPKCSFG 60
DB 1 MEPPGDMGPPPRSTPRDVLRLVLYLTFELGAPCYAPALPSCKEDEYPVGSCCPKCSFG 60
QY 61 YVKEACGELTGVCEPCPPGTYYIAHLNGLSKLCOCQMDPAMGLRASRNCSTENAVCG 120
DB 61 YVKEACGELTGVCEPCPPGTYYIAHLNGLSKLCOCQMDPAMGLRASRNCSTENAVCG 120
QY 121 CSPGHFCIVQDDHCACACRAVATSSPGORVOKGTESDTLQCNCPGTFSPNGTLEECQ 180
DB 121 CSPGHFCIVQDDHCACACRAVATSSPGORVOKGTESDTLQCNCPGTFSPNGTLEECQ 180
QY 181 HOTKCSMLVTAGAGTSSSHWMMFLSGSIVYIVCSVGLLTCVKKRRPRDVKVYVS 240
DB 181 HOTKCSMLVTAGAGTSSSHWMMFLSGSIVYIVCSVGLLTCVKKRRPRDVKVYVS 240
QY 241 VOKRQEAEGEATVIEALQAPDVTVAEETIPSTGRSPNH 283
DB 241 VOKRQEAEGEATVIEALQAPDVTVAEETIPSTGRSPNH 283

RESULT 13
US-09-886-342-60
; Sequence 60, Application US/09886342
; GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi, J.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul, J.
;; APPLICANT: Guiney, Austin, L.
;; APPLICANT: Masters, Scot, A.
;; APPLICANT: Napier, Mary, A.
;; APPLICANT: Pitti, Robert, M.
;; APPLICANT: Wood, William, I.
;; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC
;; TITLE OF INVENTION: CELL GROWTH
;; FILE REFERENCE: P2834R1PCT
;; CURRENT APPLICATION NUMBER: US/09/886,342
;; CURRENT FILING DATE: 2001-06-19
;; PRIOR APPLICATION NUMBER: 60/032,705
;; PRIOR FILING DATE: December 12, 1996
;; PRIOR APPLICATION NUMBER: 60/059,115
;; PRIOR FILING DATE: September 17, 1997
;; PRIOR APPLICATION NUMBER: 60/059,184
;; PRIOR FILING DATE: September 17, 1997
;; PRIOR APPLICATION NUMBER: 60/059,352
;; PRIOR FILING DATE: September 19, 1997
;; PRIOR APPLICATION NUMBER: 60/059,388
;; PRIOR FILING DATE: September 19, 1997
;; PRIOR APPLICATION NUMBER: 60/062,037
;; PRIOR FILING DATE: October 10, 1997
;; PRIOR APPLICATION NUMBER: 60/063,127
;; PRIOR FILING DATE: October 24, 1997
;; PRIOR APPLICATION NUMBER: 60/064,809
;; PRIOR FILING DATE: November 7, 1997
;; PRIOR APPLICATION NUMBER: 60/066,364
;; PRIOR FILING DATE: November 21, 1997
;; PRIOR APPLICATION NUMBER: 60/069,862
;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/078,004
;; PRIOR FILING DATE: March 13, 1998
;; PRIOR APPLICATION NUMBER: 60/078,936
;; PRIOR FILING DATE: March 20, 1998
;; PRIOR APPLICATION NUMBER: 60/079,728
;; PRIOR FILING DATE: March 27, 1998
;; PRIOR APPLICATION NUMBER: 60/081,071
;; PRIOR FILING DATE: April 8, 1998
;; PRIOR APPLICATION NUMBER: 60/081,954
;; PRIOR FILING DATE: April 15, 1998
;; PRIOR APPLICATION NUMBER: 60/100,858
;; PRIOR FILING DATE: September 17, 1998
;; PRIOR APPLICATION NUMBER: 60/113,296
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 60/109,304
;; PRIOR FILING DATE: November 20, 1998
;; PRIOR APPLICATION NUMBER: 60/130,232
;; PRIOR FILING DATE: April 21, 1999
;; PRIOR APPLICATION NUMBER: 60/131,022
;; PRIOR FILING DATE: April 26, 1999
;; PRIOR APPLICATION NUMBER: 60/131,445
;; PRIOR FILING DATE: April 28, 1999
;; PRIOR APPLICATION NUMBER: 60/134,287
;; PRIOR FILING DATE: May 14, 1999
;; PRIOR APPLICATION NUMBER: 60/144,758
;; PRIOR FILING DATE: July 20, 1999
;; PRIOR APPLICATION NUMBER: 60/145,698
;; PRIOR FILING DATE: July 26, 1999
;; PRIOR APPLICATION NUMBER: 08/934,494
;; PRIOR FILING DATE: September 19, 1997
;; PRIOR APPLICATION NUMBER: 08/933,821
;; PRIOR FILING DATE: September 19, 1997
;; PRIOR APPLICATION NUMBER: 08/960,507
;; PRIOR FILING DATE: October 29, 1997
;; PRIOR APPLICATION NUMBER: PCT/US97/22278
;; PRIOR FILING DATE: December 5, 1997
;; PRIOR APPLICATION NUMBER: 08/987,902
;; PRIOR FILING DATE: December 10, 1997
;; PRIOR APPLICATION NUMBER: 09/136,804
;; PRIOR FILING DATE: August 19, 1998

PRIOR APPLICATION NUMBER: 09/136,801
PRIOR FILING DATE: August 19, 1998
PRIOR APPLICATION NUMBER: 09/136,828
PRIOR FILING DATE: August 19, 1998
PRIOR APPLICATION NUMBER: 09/143,068
PRIOR FILING DATE: August 28, 1998
PRIOR APPLICATION NUMBER: 09/143,707
PRIOR FILING DATE: August 28, 1998
PRIOR APPLICATION NUMBER: PCT/US98/19093
PRIOR FILING DATE: September 14, 1998
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PRIOR FILING DATE: September 14, 1998
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/19437
PRIOR FILING DATE: September 17, 1998
PRIOR APPLICATION NUMBER: 09/169,104
PRIOR FILING DATE: October 9, 1998
PRIOR APPLICATION NUMBER: PCT/US98/21407
PRIOR FILING DATE: October 9, 1998
PRIOR APPLICATION NUMBER: PCT/US98/24855
PRIOR FILING DATE: November 20, 1998
PRIOR APPLICATION NUMBER: 09/202,088
PRIOR FILING DATE: December 8, 1998
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PRIOR APPLICATION NUMBER: PCT/US99/00106
PRIOR FILING DATE: January 5, 1999
PRIOR APPLICATION NUMBER: 09/254,465
PRIOR FILING DATE: March 5, 1999
PRIOR APPLICATION NUMBER: PCT/US99/05028
PRIOR FILING DATE: March 8, 1999
PRIOR APPLICATION NUMBER: 09/254,460
PRIOR FILING DATE: March 9, 1999
PRIOR APPLICATION NUMBER: 09/284,291
PRIOR FILING DATE: April 12, 1999
PRIOR APPLICATION NUMBER: 09/332,928
PRIOR FILING DATE: June 14, 1999
PRIOR APPLICATION NUMBER: 09/332,929
PRIOR FILING DATE: June 14, 1999
PRIOR APPLICATION NUMBER: 09/333,075
PRIOR FILING DATE: June 14, 1999
PRIOR APPLICATION NUMBER: 09/333,077
PRIOR FILING DATE: June 14, 1999
PRIOR APPLICATION NUMBER: 09/380,138
PRIOR FILING DATE: August 25, 1999
PRIOR APPLICATION NUMBER: 09/380,139
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PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: 09/403,296
PRIOR FILING DATE: October 18, 1999
PRIOR APPLICATION NUMBER: 09/423,844
PRIOR FILING DATE: November 12, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: November 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: December 2, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/31274
PRIOR FILING DATE: December 30, 1999
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: January 5, 2000
PRIOR APPLICATION NUMBER: PCT/US00/00277
PRIOR FILING DATE: January 6, 2000
PRIOR APPLICATION NUMBER: 09/480,284
PRIOR FILING DATE: January 10, 2000
PRIOR APPLICATION NUMBER: PCT/US00/03565

PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04341
PRIOR FILING DATE: February 18, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: 09/511,133
PRIOR FILING DATE: February 23, 2000
PRIOR APPLICATION NUMBER: 09/511,631
PRIOR FILING DATE: February 23, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/06884
PRIOR FILING DATE: March 15, 2000
PRIOR APPLICATION NUMBER: PCT/US00/07377
PRIOR FILING DATE: March 20, 2000
PRIOR APPLICATION NUMBER: PCT/US00/07532
PRIOR FILING DATE: March 21, 2000
PRIOR APPLICATION NUMBER: PCT/US00/13705
PRIOR FILING DATE: May 17, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/15264
PRIOR FILING DATE: June 2, 2000
PRIOR APPLICATION NUMBER: 09/664,610
PRIOR FILING DATE: September 18, 2000
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: September 18, 2000
PRIOR APPLICATION NUMBER: 09/690,169
PRIOR FILING DATE: October 16, 2000
PRIOR APPLICATION NUMBER: 09/690,189
PRIOR FILING DATE: October 16, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: 09/808,689
PRIOR FILING DATE: March 14, 2001
NUMBER OF SEQ ID NOS: 79
SEQ ID NO 60
LENGTH: 283
TYPE: PRT
ORGANISM: Homo Sapien
US-09-886-342-60

Query Match 100.0%; Score 1578; DB 22; Length 283;
Best Local Similarity 100.0%; Pred. No. 3,66-119;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MEPPGDMGPPPMWSTPRTDVLRLVLTFLGAPCYAPALPCKEDEXYPVGSCECCPKSPG 60

QY 61 YRKKEAGCELGTGVCPCPGTYIAHLNLSKLCQCMCDPMGLASRNCSTENAVCG 120
Db 61 YRKKEAGCELGTGVCPCPGTYIAHLNLSKLCQCMCDPMGLASRNCSTENAVCG 120

QY 121 CSRGHCIVQDDGDHCAACRAVATSSPGQVROKGGTESODTLONCPGTFSPNGTLEBQ 180
Db 121 CSRGHCIVQDDGDHCAACRAVATSSPGQVROKGGTESODTLONCPGTFSPNGTLEBQ 180

QY 181 HQTCKSMVLTAKAGAGTSSSHWMMFLSGSLVIVYVSTVGLIICVARRRPRGDVYKVIYS 240
Db 181 HQTCKSMVLTAKAGAGTSSSHWMMFLSGSLVIVYVSTVGLIICVARRRPRGDVYKVIYS 240

QY 241 VORRROEAGEATVIEALQAPPDVTTVAVEETIPSTGRSPNH 283
Db 241 VORRROEAGEATVIEALQAPPDVTTVAVEETIPSTGRSPNH 283

RESULT 14
US-09-935-727-31
Sequence 31, Application US/09935727
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.

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: TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
: FILE REFERENCE: PF454P2
: CURRENT APPLICATION NUMBER: US/09/935,727
: CURRENT FILING DATE: 2001-08-24
: PRIOR APPLICATION NUMBER: 60/303,224
: PRIOR FILING DATE: 2001-07-06
: PRIOR APPLICATION NUMBER: 60/252,131
: PRIOR FILING DATE: 2000-11-21
: PRIOR APPLICATION NUMBER: 60/227,598
: PRIOR FILING DATE: 2000-08-25
: PRIOR APPLICATION NUMBER: 09/518,931
: PRIOR FILING DATE: 2000-03-03
: PRIOR APPLICATION NUMBER: 60/168,235
: PRIOR FILING DATE: 1999-12-01
: PRIOR APPLICATION NUMBER: 60/146,371
: PRIOR FILING DATE: 1999-08-02
: PRIOR APPLICATION NUMBER: 60/131,964
: PRIOR FILING DATE: 1999-04-30
: PRIOR APPLICATION NUMBER: 60/131,270
: PRIOR FILING DATE: 1999-04-27
: PRIOR APPLICATION NUMBER: 60/124,092
: PRIOR FILING DATE: 1999-03-12
: PRIOR APPLICATION NUMBER: 60/121,774
: PRIOR FILING DATE: 1999-03-04
: PRIOR APPLICATION NUMBER: 09/006,352
: PRIOR FILING DATE: 1998-01-13
: PRIOR APPLICATION NUMBER: 60/035,496
: PRIOR FILING DATE: 1997-01-14
: NUMBER OF SEQ ID NOS: 42
: SOFTWARE: Patent In Ver. 2.1
: SEQ ID NO: 31
: LENGTH: 283
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-935-727-31
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Query Match 100.0%; Score 1578; DB 23; Length 283;

Best Local Similarity 100.0%; Pred. No. 3.6e-119; Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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    |||||||
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QY 61 YRVKACGELTGTVCPCPGTYIAHLNGLSKLCCQCMCDPAMGLRASNCSRTENAVCG 120
    |||||||
DB 61 YRVKACGELTGTVCPCPGTYIAHLNGLSKLCCQCMCDPAMGLRASNCSRTENAVCG 120
QY 121 CSPGHFCIVODDHCACRAVATSSPGQVROKGTESODTLCONCPGTFSPNGTLEECQ 180
    |||||||
DB 121 CSPGHFCIVODDHCACRAVATSSPGQVROKGTESODTLCONCPGTFSPNGTLEECQ 180
QY 181 HOTKCSMLVTKAGAGTSSSHWMMFLSGSLVIVYICSTYGLIICVRRKPRDGVKVIYS 240
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DB 181 HOTKCSMLVTKAGAGTSSSHWMMFLSGSLVIVYICSTYGLIICVRRKPRDGVKVIYS 240
QY 241 VORRROEAGEATVIEALQAPPDVTVVAEETIPSTGSRPNH 283
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DB 241 VORRROEAGEATVIEALQAPPDVTVVAEETIPSTGSRPNH 283
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RESULT 15

PCT-US96-18540-2

; Sequence 2, Application PC/TUS9618540

; GENERAL INFORMATION:

; APPLICANT: Human Genome Sciences, Inc.

; APPLICANT: 9410 Key West Avenue

; APPLICANT: Rockville, MD 20850

; APPLICANT: United States of America

; APPLICANT: 709 Swedeland Road

; APPLICANT: King of Prussia, PA 19406

; APPLICANT: United States of America

```

: APPLICANT: Rosen, Craig A.
: APPLICANT: Gentz, Reiner L.
: APPLICANT: Lynn, Sally Doreen Patricia
: APPLICANT: Hurlie, Mark Robert
: TITLE OF INVENTION: Human Tumor Necrosis Factor
: NUMBER OF SEQUENCES: 24
: CORRESPONDENCE ADDRESS:
: ADDRESSER: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
: STREET: 1100 New York Ave, Suite 600
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20005-3934
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US96/18540
: FILING DATE: Herewith
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Goldstein, Jorge A.
: REGISTRATION NUMBER: 29,021
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-271-2540
: TELEFAX: 202-271-2540
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 283 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
PCT-US96-18540-2
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Query Match 99.8%; Score 1575; DB 1; Length 283;

Best Local Similarity 99.6%; Pred. No. 6.2e-119; Matches 282; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 181 HOTKCSMLVTKAGAGTSSSHWMMFLSGSLVIVYICSTYGLIICVRRKPRDGVKVIYS 240
QY 241 VORRROEAGEATVIEALQAPPDVTVVAEETIPSTGSRPNH 283
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DB 241 VORRROEAGEATVIEALQAPPDVTVVAEETIPSTGSRPNH 283
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Search completed: January 24, 2002, 16:24:29

Job time: 194 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 24, 2002, 16:21:15 ; Search time 13.38 Seconds
(without alignments)
735.450 Million cell updates/sec

Title: US-08-741-095B-26

Perfect score: 1578
Sequence: 1 MEPPDGMGPPWRSTPRDTV.....VTVVAVERTPSTGRSPNH 283

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 160442 seqs, 34771459 residues

Total number of hits satisfying chosen parameters: 160442

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_New:*
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2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1578	100.0	283	5	US-09-924-231-2
2	1073	68.0	419	5	US-09-924-231-7
3	267.5	17.0	277	5	US-09-855-528-2
4	259	16.4	184	5	US-09-852-455-8
5	259	16.4	225	5	US-09-840-795-10
6	259	16.4	237	5	US-09-579-845-10
7	259	16.4	461	5	US-09-896-096A-17
8	259	16.4	518	5	US-09-579-845-1
9	259	16.4	518	5	US-09-579-845-3
10	246	15.6	300	5	US-09-896-096A-1
11	239	15.1	300	5	US-09-840-795-2
12	230.3	14.6	197	6	US-10-003-211-1
13	221	14.0	487	5	US-09-579-845-14
14	217	13.8	258	5	US-09-579-845-7
15	213.5	13.5	227	5	US-09-840-795-9
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23	208.5	13.2	591	5	US-09-877-650-2
24	208.5	13.2	622	5	US-09-957-944-10
25	206	13.1	335	5	US-09-949-713-20
26	205	13.0	444	5	US-09-840-795-8

27	205	13.0	655	5	US-09-978-189-64	Sequence 64, Appl
28	205	13.0	655	5	US-09-978-192-64	Sequence 64, Appl
29	205	13.0	655	5	US-09-978-657-64	Sequence 64, Appl
30	205	13.0	655	5	US-09-978-824-64	Sequence 64, Appl
31	205	13.0	655	5	US-09-840-795-6	Sequence 6, Appl
32	203.5	12.9	251	5	US-09-821-831-4	Sequence 4, Appl
33	203.5	12.9	425	5	US-09-821-831-2	Sequence 2, Appl
34	200.5	12.7	258	5	US-09-579-845-8	Sequence 8, Appl
35	198.5	12.6	625	5	US-09-957-944-4	Sequence 4, Appl
36	198.5	12.6	625	5	US-09-877-650-15	Sequence 15, Appl
37	191	12.1	176	5	US-09-892-100-18	Sequence 18, Appl
38	186	11.8	128	5	US-09-949-713-9	Sequence 9, Appl
39	186	11.8	143	5	US-09-949-713-10	Sequence 10, Appl
40	186	11.8	144	5	US-09-949-713-21	Sequence 21, Appl
41	186	11.8	157	5	US-09-949-713-15	Sequence 15, Appl
42	186	11.8	159	5	US-09-949-713-23	Sequence 23, Appl
43	186	11.8	360	5	US-09-949-713-11	Sequence 11, Appl
44	186	11.8	376	5	US-09-949-713-22	Sequence 22, Appl
45	185.5	11.8	210	5	US-09-840-795-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-09-924-231-2
Sequence 2, Application US/09924231
GENERAL INFORMATION:
APPLICANT: SPEAR, Patricia G.
APPLICANT: MONTGOMERY, Rebecca I.
TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
FILE REFERENCE: 0290-1
CURRENT APPLICATION NUMBER: US/09/924,231
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 09/333,279
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 283
TYPE: PRT
ORGANISM: Homo sapiens
US-09-924-231-2

Query Match	100.0%	Score 1578:	DB 5:	Length 283:
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DB	1	MEPPDGMGPPWRSTPRDTVRLVLTFLGAPCYAPALPSCKEDEYVGSCECPKSPG	60	
QY	61	YRVKACGELTGTVCPCPGTYIAHLNGLSKLCLOCMCDPAMGLRASRNCSTENAVCG	120	
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DB	121	CSPGHFCIVDGDHCAACRAVATSSPGORVOKGTESODTLQNCPCPTFSFNGTLEECQ	180	
QY	181	HOTKSMVLTAKAGTSSSHWVWFLSGSLVIVYICVSVGLICVKKRRPRCDVVKVYS	240	
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DB	241	VQRKQAEAGATVIEALQAPPDVTVAVEETIPSTGRSPNH	283	
RESULT 2				
US-09-924-231-7				
Sequence 7, Application US/09924231				

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GENERAL INFORMATION:
APPLICANT: SPEAR, Patricia G.
APPLICANT: MONTGOMERY, Rebecca I.
TITLE OF INVENTION: HERPES VIRUS ENTRY RECEPTOR PROTEIN
FILE REFERENCE: 0290-1
CURRENT APPLICATION NUMBER: US/09/924,231
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 09/333,279
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 7
LENGTH: 419
TYPE: PRT
ORGANISM: Homo sapiens
US-09-924-231-7
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Best Local Similarity 100.0%; Pred. No. 2,1e-85;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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    |||||
DB 61 YVKEACGELTGVCPECPGTIYIAHLNGLSKLCCOMCDPMGLRASRNCSTENAAGC 120
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DB 121 CSPGHFCIVQDDHCAACRAVATSSPGORVOKGTEGSDTLCONCPPTGSPNGTLEECQ 180
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DB 181 HOTKC 185
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RESULT 3
US-09-855-528-2
Sequence 2, Application US/09855528
GENERAL INFORMATION:
APPLICANT: NOELLE, RANDOLPH J.
APPLICANT: BURNS, CHRISTOPHER M.
TITLE OF INVENTION: USE OF ANTI-GP-39 ANTIBODIES FOR TREATMENT AND/OR
TITLE OF INVENTION: REVERSAL OF LUPUS AND LUPUS ASSOCIATED KIDNEY DISEASE
FILE REFERENCE: 037003-0280622
CURRENT APPLICATION NUMBER: US/09/855,528
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 09/054,488
PRIOR FILING DATE: 1998-04-03
PRIOR APPLICATION NUMBER: 08/742,480
PRIOR FILING DATE: 1996-11-01
PRIOR APPLICATION NUMBER: 08/338,975
PRIOR FILING DATE: 1994-11-14
PRIOR APPLICATION NUMBER: 07/835,799
PRIOR FILING DATE: 1992-02-14
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 2
LENGTH: 277
TYPE: PRT
ORGANISM: Homo sapiens
US-09-855-528-2
```

```
Query Match      17.0%; Score 267.5; DB 5; Length 277;
Best Local Similarity 26.1%; Pred. No. 5.5e-16;
Matches 71; Conservative 50; Mismatches 116; Indels 35; Gaps 9;
```

```
DB 1 MWRLPLOCVLMG--CLTAVHPEPTACREKQYLINSQCCSLCQPOQKLVSDCTEFTETE 58
OY 75 CEPCPGGTIAHLNGLSKLCCOMCDPMGLRASRNCSTENAAGCCSGHFCIVQDDGH 134
    |||||
DB 59 CLPCGSEFLDYNRRTHOHRKYCDPNGLVQVQGISSETPTICTCEGHWGC---TSEA 115
OY 135 CAACRAVATSSPGORVOKGTEGSDTLCONCPPTGFS-PNGTLEECQHOTKCSW--LVTK 191
    |||||
DB 116 CESCIVLRSCSGFGVKQATGVSDTICPCPVGFSSNVSAFECHPMTSCETDLYVQ 175
OY 192 AGAGTSSSHWVWVFLGSLVIVICSTVGLIIVARRKRGDGVKVIYSVQRRQDAEGE 251
    |||||
DB 176 Q-AGTNKTDVVCQPDRLRALVIRPIIFGILPA-----ILVLVFIKRVAKKPTNK 225
OY 252 ATVIELQAPPVY-----TVAVGETI 273
DB 226 AP--HPKQEPQEIPEPDDLPGSKTAPVQETL 255
```

```
RESULT 4
US-09-852-455-8
Sequence 8, Application US/09852455
GENERAL INFORMATION:
APPLICANT: BLUME, ARTHUR J.
APPLICANT: GOLDSTEIN, NEIL
APPLICANT: PILUTA, RENYU
APPLICANT: HSINO, KU-CHUAN
APPLICANT: PRENDERGAST, JOHN
TITLE OF INVENTION: METHODS OF IDENTIFYING THE ACTIVITY OF GENE PRODUCTS
FILE REFERENCE: 2598-4004051
CURRENT APPLICATION NUMBER: US/09/852,455
CURRENT FILING DATE: 2001-05-09
PRIOR APPLICATION NUMBER: 60/202,912
PRIOR FILING DATE: 2000-05-09
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 8
LENGTH: 184
TYPE: PRT
ORGANISM: Homo sapiens
US-09-852-455-8
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Query Match      16.4%; Score 259; DB 5; Length 184;
Best Local Similarity 32.8%; Pred. No. 2e-15;
Matches 59; Conservative 23; Mismatches 76; Indels 22; Gaps 6;
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```
OY 35 YAPALPS-CKEDEV--PVGECCPKCSFGYRVKACGELTGVCPECPGTIYIAHLNGLS 91
    |||||
DB 10 YAPEPGSTCRLREYYDQTAOMCCSKCSPGOHAKVCFCTISDVCDSCBDSYVTLMMVVP 69
OY 92 KCLCCOMCDPMGLRASRNCSTENAAGCCSGHFCIVQDDGHCAACRAVATSS 145
    |||||
DB 70 ECLSC-----GSRCSDDQVETQACTREONRITCRGRGWCALSKQGCRCALPRLRCR 122
OY 146 PGQORVOKGTEGSDTLCONCPPTGFS-PNGTLEECQHOTKCSWLTAKAGAG-----TSSS 199
    |||||
DB 123 PGFGVARGTETISDVYCAKPCAPAGTFSNTTSTIDICRHOICNVVAIPQNASRDAVCTSTS 182
```

```
RESULT 5
US-09-840-795-10
Sequence 10, Application US/09840795
GENERAL INFORMATION:
APPLICANT: Murphy, Erin E.
APPLICANT: Mattison, Jeanine D.
APPLICANT: Bates, Elizabeth Esther Mary
APPLICANT: Gorman, Daniel M.
APPLICANT: Lebecque, Serge J.E.
TITLE OF INVENTION: Mammalian Genes: Related Reagents
FILE REFERENCE: SF0818K
CURRENT APPLICATION NUMBER: US/09/840,795
CURRENT FILING DATE: 2001-04-23
```



```
; PRIOR APPLICATION NUMBER: 09/351,777
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 10
; LENGTH: 225
; TYPE: PRT
; ORGANISM: primate
US-09-840-795-10

Query Match
16.4%; Score 259; DB 5; Length 225;
Best Local Similarity 32.8%; Pred. No. 2.4e-15;
Matches 59; Conservative 23; Mismatches 76; Indels 22; Gaps 6;

OY 35 YAPALPS-CKEDEV--PVGSECCPKCSPGYRKKEACGELTGVCPCPGTYIAHLNGLS 91
DB 32 YAPBGSCTRLREYDQTAQOMCCSKSPQAHKVCCTSDVDCSCDSTYTQLMNWP 91
OY 92 KLOCOMDPAWGLRASHN-----CSRTENAVCGSPGHFCIVODGDHCAACRAVATSS 145
DB 92 ECLSC-----GSRCSQVETQACTREQNRICTRRGWICALSKQECRCRLCAPLRKCR 144
OY 146 PGQRYOKGOTESQDTLCONCPGTFPS-PNGTLEECQHOHCKCSMLVTKAGAG-----TSSS 199
DB 145 PGFGVAPRGTESTDVYCKPCAPGTFPSNTTSTDICRPHQICNVVAIPGNASMDAVCTSTS 204

RESULT 6
US-09-579-845-10
; Sequence 10, Application US/09579845
; GENERAL INFORMATION:
; APPLICANT: Bursfeldt, Haim
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOWERING
; TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS FACTOR (TNF) IN TNF-ASSOCIATED
; FILE REFERENCE: 226272004420
; CURRENT APPLICATION NUMBER: US/09/579,845
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/150,688
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-579-845-10

Query Match
16.4%; Score 259; DB 5; Length 257;
Best Local Similarity 32.8%; Pred. No. 2.8e-15;
Matches 59; Conservative 23; Mismatches 76; Indels 22; Gaps 6;

OY 35 YAPALPS-CKEDEV--PVGSECCPKCSPGYRKKEACGELTGVCPCPGTYIAHLNGLS 91
DB 32 YAPBGSCTRLREYDQTAQOMCCSKSPQAHKVCCTSDVDCSCDSTYTQLMNWP 91
OY 92 KLOCOMDPAWGLRASHN-----CSRTENAVCGSPGHFCIVODGDHCAACRAVATSS 145
DB 92 ECLSC-----GSRCSQVETQACTREQNRICTRRGWICALSKQECRCRLCAPLRKCR 144
OY 146 PGQRYOKGOTESQDTLCONCPGTFPS-PNGTLEECQHOHCKCSMLVTKAGAG-----TSSS 199
DB 145 PGFGVAPRGTESTDVYCKPCAPGTFPSNTTSTDICRPHQICNVVAIPGNASMDAVCTSTS 204

RESULT 7
US-09-896-096A-17
; Sequence 17, Application US/09896096A
; GENERAL INFORMATION:
; APPLICANT: ASHKENAZI, AVI J
```

```
; APPLICANT: BOTSTEIN, DAVID
; APPLICANT: DODGE, KELLY H.
; APPLICANT: GURNEY, AUSTIN L.
; APPLICANT: KIM, KYUNG JIN
; APPLICANT: LAWRENCE, DAVID A.
; APPLICANT: PITTI, ROBERT
; APPLICANT: ROY, MARGARET A
; APPLICANT: THOMAS, DANIEL B
; APPLICANT: WOOD, WILLIAM I.
; TITLE OF INVENTION: DCR3 Polypeptide, A TNFR Homolog
; FILE REFERENCE: P1134R2 REVISED
; CURRENT APPLICATION NUMBER: US/09/896,096A
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/157,289
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: US 60/059,288
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: US 60/094,640
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 17
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-896-096A-17

Query Match
16.4%; Score 259; DB 5; Length 461;
Best Local Similarity 32.8%; Pred. No. 4.9e-15;
Matches 59; Conservative 23; Mismatches 76; Indels 22; Gaps 6;

OY 35 YAPALPS-CKEDEV--PVGSECCPKCSPGYRKKEACGELTGVCPCPGTYIAHLNGLS 91
DB 32 YAPBGSCTRLREYDQTAQOMCCSKSPQAHKVCCTSDVDCSCDSTYTQLMNWP 91
OY 92 KLOCOMDPAWGLRASHN-----CSRTENAVCGSPGHFCIVODGDHCAACRAVATSS 145
DB 92 ECLSC-----GSRCSQVETQACTREQNRICTRRGWICALSKQECRCRLCAPLRKCR 144
OY 146 PGQRYOKGOTESQDTLCONCPGTFPS-PNGTLEECQHOHCKCSMLVTKAGAG-----TSSS 199
DB 145 PGFGVAPRGTESTDVYCKPCAPGTFPSNTTSTDICRPHQICNVVAIPGNASMDAVCTSTS 204

RESULT 8
US-09-579-845-1
; Sequence 1, Application US/09579845
; GENERAL INFORMATION:
; APPLICANT: Bursfeldt, Haim
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOWERING
; TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS FACTOR (TNF) IN TNF-ASSOCIATED
; FILE REFERENCE: 226272004420
; CURRENT APPLICATION NUMBER: US/09/579,845
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/150,688
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-579-845-1

Query Match
16.4%; Score 259; DB 5; Length 518;
Best Local Similarity 32.8%; Pred. No. 5.5e-15;
Matches 59; Conservative 23; Mismatches 76; Indels 22; Gaps 6;

OY 35 YAPALPS-CKEDEV--PVGSECCPKCSPGYRKKEACGELTGVCPCPGTYIAHLNGLS 91
DB 32 YAPBGSCTRLREYDQTAQOMCCSKSPQAHKVCCTSDVDCSCDSTYTQLMNWP 91
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```

Db 61 YAPEPSTGRLREYDQTAQMCCSKSPGQHAKEFTKTSDFVCDSECDSTYTQLMNVWP 120
QY 92 KCLQCCMCPDPMGLRASRN-----CSRTENAVCGSPGHEFCIVQGDHCAACRAVATSS 145
Db 121 ECLSC-----GSRCSDDVETQACTREONRITCTCRPGWYCALSKOEGCRICAPLRKCR 173
QY 146 PGQRVQKGTESODTLQONCPPTGFS--PNGTLECOHQTKCSWLVTKAGAG-----TSSS 199
Db 174 PGCGVARPGTETSDVYCKPCAPGTFSTNTSTDICRPHQICNVVAIPGNASMDAVCTSTS 233

RESULT 9
US-09-579-845-3
; Sequence 3, Application US/09579845
; GENERAL INFORMATION:
; APPLICANT: Birstein, Haim
; APPLICANT: Stepan, Anthony M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR LOWERING
; TITLE OF INVENTION: THE LEVEL OF TUMOR NECROSIS FACTOR (TNF) IN TNF-ASSOCIATED
; FILE REFERENCE: 226272004420
; CURRENT APPLICATION NUMBER: US/09/579,845
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/150,688
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-579-845-3

```

```

Query Match 16.4%; Score 259; DB 5; Length 518;
Best Local Similarity 32.8%; Pred. No. 5.5e-15;
Matches 59; Conservative 23; Mismatches 76; Indels 22; Gaps 6;

QY 35 YAPALPS-CKEDFY--PVSECCPKSPGYRVKACGELTGVCPCPPGTATIAHLNGLS 91
Db 61 YAPEPSTGRLREYDQTAQMCCSKSPGQHAKEFTKTSDFVCDSECDSTYTQLMNVWP 120
QY 92 KCLQCCMCPDPMGLRASRN-----CSRTENAVCGSPGHEFCIVQGDHCAACRAVATSS 145
Db 121 ECLSC-----GSRCSDDVETQACTREONRITCTCRPGWYCALSKOEGCRICAPLRKCR 173
QY 146 PGQRVQKGTESODTLQONCPPTGFS--PNGTLECOHQTKCSWLVTKAGAG-----TSSS 199
Db 174 PGCGVARPGTETSDVYCKPCAPGTFSTNTSTDICRPHQICNVVAIPGNASMDAVCTSTS 233

```

```

RESULT 10
US-09-896-096A-1
; Sequence 1, Application US/09896096A
; GENERAL INFORMATION:
; APPLICANT: ASHKENAZI, AVI J
; APPLICANT: BOTSTEIN, DAVID
; APPLICANT: DODGE, KELLY H.
; APPLICANT: GURNEY, AUSTIN L.
; APPLICANT: KIM, KYUNG JIN
; APPLICANT: LAWRENCE, DAVID A.
; APPLICANT: PITTI, ROBERT
; APPLICANT: ROY, MARGARET A
; APPLICANT: TUMAS, DANIEL B
; APPLICANT: WOOD, WILLIAM I.
; TITLE OF INVENTION: DCR3 Polyptide, A TNFR Homolog
; FILE REFERENCE: P1134R2 REVISED
; CURRENT APPLICATION NUMBER: US/09/896,096A
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/157,289
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: US 60/059,288
; PRIOR FILING DATE: 1997-09-18

```

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; PRIOR APPLICATION NUMBER: US 60/094,640
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 1
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-896-096A-1

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```

Query Match 15.6%; Score 246; DB 5; Length 300;
Best Local Similarity 35.4%; Pred. No. 4.3e-14;
Matches 69; Conservative 16; Mismatches 88; Indels 22; Gaps 8;

QY 16 PRIDVLRVLVLYFLGAPCYAPALPSCKE--DEP-----VGSE--CCPKSPGYRVKACG 68
Db 7 PGLSLCLVLALPAL--LPVPAVRGVAETPPYPMWDAETGRLVCAOCPPTGFVQRPDR 63
QY 69 ELTGVCCEPCPPGTATIAHLNGLSKCLQCCMCPDPMGLR--ASRNCSTRTENAVCGSPGHF 126
Db 64 RDSPTTCGCPFRHHTYQFNLYER---CRXCNVLCGEREEBARACHATINRACRCRTGTF 120
QY 127 CIVQDGDHCAACRAVATSSPGQRVQKGTESODTLQONCPPTGFS--PNGTLECOHQTKC 185
Db 121 A-----HAGFCLCHASCPGAGVIAPGTPSQWTCQPCPPGTFSSASSSSSCOPHRNC 174
QY 186 SWLVTKAGAGTSSSH 200
Db 175 TALGLALNVPGSSSH 189

```

```

RESULT 11
US-09-840-795-2
; Sequence 2, Application US/09840795
; GENERAL INFORMATION:
; APPLICANT: Murphy, Erin E.
; APPLICANT: Mattson, Jeanine D.
; APPLICANT: Bates, Elizabeth Esther Mary
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Lebecque, Serge J.E.
; TITLE OF INVENTION: Mammalian Genes; Related Reagents
; FILE REFERENCE: SF0818K
; CURRENT APPLICATION NUMBER: US/09/840,795
; CURRENT FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 09/351,777
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 300
; TYPE: PRT
; ORGANISM: primate
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (79)
; OTHER INFORMATION: Xaa at residue 79 is undetermined.
US-09-840-795-2

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```

Query Match 15.1%; Score 239; DB 5; Length 300;
Best Local Similarity 35.2%; Pred. No. 1.7e-13;
Matches 69; Conservative 15; Mismatches 88; Indels 24; Gaps 9;

QY 16 PRIDVLRVLVLYFLGAPCYAPALPSCKE--DEP-----VGSE--CCPKSPGYRVKACG 68
Db 7 PGLSLCLVLALPAL--LPVPAVRGVAETPPYPMWDAETGRLVCAOCPPTGFVQRPDR 63
QY 69 ELTGVCCEPCPPGTATIAHLNGLSKCLQCCMCPDPMGLR--ASRNCSTRTENAVCGSPGHF 125
Db 64 RDSPTTCGCPFRHHTYQFNLYERCHXCYVLC-----GEREEBARACHATINRACRCRTG 119
QY 126 CIVQDGDHCAACRAVATSSPGQRVQKGTESODTLQONCPPTGFS--PNGTLECOHQTKC 184

```



```

RESULT 15
US-09-840-795-9
; Sequence 9 Application US/09840795
; GENERAL INFORMATION:
; APPLICANT: Murphy, Erin E.
; APPLICANT: Mattson, Jeanine D.
; APPLICANT: Bates, Elizabeth Esther Mary
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Lebecque, Serge J. E.
; TITLE OF INVENTION: Mammalian Genes; Related Reagents
; FILE REFERENCE: SF0818K
; CURRENT APPLICATION NUMBER: US/09/840,795
; CURRENT FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 09/351,777
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 227
; TYPE: prt
; ORGANISM: rodent
US-09-840-795-9

```

```

Query Match 13.5%; Score 213.5; DB 5; Length 227;
Best local Similarity 28.5%; Pred. No. 2,1e-11;
Matches 55; Conservative 20; Mismatches 101; Indels 17; Gaps 6;

QY 20 VRLVLYLFLGAPCYAPALPSCKEDEY--PVGSE-----CCPKCSPGYRVKEAGE 69
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 11 VFELQIMATGHTVPAOVVLTLPYKPEPGYECQISQEYVDRKQKCAKCPGQYVKKHFCNK 70
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 70 LRGTVCEPCPGTYIHLNGLSKLOC--QMDPAMGLASRNCSTENAVCGCSPGHFC 127
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 71 TSDTVACDEASMTQVWNOFTCLSCSSSCTTDOVEIRA--CTKQONRVCACEAGRYC 127
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 128 IVO-DDDHCAACRAVATSSPGQVROKGTESODTLCNCPPTGFS--PNGTLEECQHQTGC 185
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 128 ALKTHGSGRCQMRSLKCGPGFGVASSRAPNGNVLCACAPGTFTSTSDVCRPHRIC 187
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 186 SWLVTKAGAGTSS 198
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 188 SILAIPGNASTDA 200
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

Search completed: January 24, 2002, 16:22:45
 Job time: 90 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 24, 2002, 16:21:10 ; Search time 16.49 Seconds

(without alignments)
1307.301 Million cell updates/sec

Title: US-08-741-095b-26

Perfect score: 1578

Sequence: 1 MEPPGDMGPPMRSPTDY.....VTVAVEETIPSTGSPNH 283

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : PIR_68:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	276.5	17.5	305	2 A66476	B cell-associated
2	267.5	17.0	277	2 A60771	B-cell activation
3	260	16.5	325	2 B43692	T2 protein - rabd1
4	259	16.4	461	1 A45356	tumor necrosis fac
5	257.5	16.3	348	2 T28623	hypothetical prote
6	257	16.3	349	2 D72175	G2R protein - vari
7	257	16.3	349	2 D36858	gene G4R protein -
8	253	16.0	435	2 T54182	tumor necrosis fac
9	240.5	15.2	271	2 S12783	OX40 antigen precu
10	238.5	15.1	326	1 GQVZML	T2 protein - myxom
11	215.5	13.7	272	2 I48700	gene ox40 protein
12	213.5	13.5	474	2 B38634	tumor necrosis fac
13	212.5	13.5	459	2 I48854	gene murine tumor
14	206.5	13.1	324	2 J02395	Fas antigen precu
15	206	13.1	335	2 A40036	apoptosis-mediati
16	205	13.0	327	2 A46484	apoptosis-mediati
17	203.5	12.9	425	1 A26431	nerve growth facto
18	198.5	12.6	416	1 JN0006	nerve growth facto
19	194.5	12.3	277	2 I37552	OX40 homolog - hum
20	192	12.2	461	1 GORWT1	tumor necrosis fac
21	190	12.0	427	1 GORUN	nerve growth facto
22	186	11.8	314	2 I37383	FAS soluble protei
23	176.5	11.2	256	2 B32393	T-cell antigen 4-1
24	172.5	10.9	461	2 J04302	tumor necrosis fac
25	171	10.8	250	1 A49053	CD27 antigen precu
26	168.5	10.7	454	1 GOMST1	tumor necrosis fac
27	161	10.2	255	2 I38426	lymphocyte activat
28	159	10.1	595	2 A42086	CD30 antigen precu
29	155	9.8	455	1 GQHUT1	tumor necrosis fac

30	148	9.4	260	1 A46517	CD27 antigen precu
31	144.5	9.2	493	2 J05486	membrane glycoprot
32	143.5	9.1	1786	1 MMHUB1	laminin beta-1 cha
33	139.5	8.8	5376	2 T42215	zonadhesin - mouse
34	135.5	8.6	1274	2 T42017	cysteine rich prot
35	135	8.6	1574	2 T13954	MEGF6 protein - ra
36	134	8.5	2824	2 T22759	hypothetical prote
37	133.5	8.5	4391	2 A38096	perlecan precursor
38	130.5	8.3	1786	1 MMMSB1	laminin beta-1 cha
39	128.5	8.1	2533	2 T28675	alpha-5ID immobill
40	128.5	8.1	2533	2 T28674	variant-specific s
41	127.5	8.1	596	2 A45664	hypothetical prote
42	127.5	8.1	1372	2 T25933	heparan sulfate pr
43	127.5	8.1	3707	2 S18252	laminin beta-2 cha
44	127	8.0	1797	2 A55677	laminin beta-2 cha
45	127	8.0	1798	2 S53869	laminin beta-2 cha

ALIGNMENTS

```
RESULT 1
A46476
B cell-associated surface molecule CD40, long splice form - mouse
C:Species: Mus musculus (house mouse)
C>Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
C:Accession: A46476; A46515
R:Torres, R.M.; Clark, E.A.
J. Immunol. 148, 620-626, 1992
A:Title: Differential increase of an alternatively polyadenylated mRNA species of mur
A:Reference number: A46476; MUID:92105763
A:Accession: A46476
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-305 <TOR>
A:Cross-references: GB:M83312; NID:g1553058
A>Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBI:75207)
A>Note: this translation is not annotated in GenBank entry M83312, release 113.0
R:Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockay
J. Immunol. 149, 3921-3926, 1992
A:Title: Genomic structure and chromosomal mapping of the murine CD40 gene.
A:Reference number: A46515; MUID:93094586
A:Accession: A46515
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-287, "LV" <GR1>
A:Cross-references: GB:M83312; NID:g1553058; PIDN:AAB08705.1; PID:g1553059; GB:M94126
A:Experimental source: BALB/c, liver
A>Note: sequence extracted from NCBI backbone (NCBI:120357)
C:Comment: For an alternative splice form, see PIR:A46515.
C:Comment: For an alternative splice form, see PIR:A46476.
C:Superfamily: CD27 antigen; NCF receptor repeat homology
C:Keywords: alternative splicing; transmembrane protein
F:105-144/Domains: NGF receptor repeat homology <NGF>

Query Match 17.5%; Score 276.5; DB 2; Length 305;
Best Local Similarity 27.9%; Pred. No. 2.9e-13;
Matches 69; Conservative 43; Mismatches 106; Indels 29; Gaps 8;
```

```
OY 1 SCKEDYVPGSECPKCPGVRKACGELNGTVCPEPCPGPYIAHLNGLSKLQCCOMCD 100
DB 25 TCSDDQVYLDQCCDCLQPGSRSLTSHCALFETQCHPCDSCGFSQWNRREIRCHQHRICE 84
OY 101 PAMGLRASRNCSTRENAVCGSPGHFCTVODGDHCACRAYATSSPGQVRQKGTESODT 160
DB 85 PNQGLRVRKKEGAEEDYCTCEKEGCHTCKSD--CEACAQHPICIPRGVEMARETDT 141
OY 161 LCQNPPTGTFSPNGTL-EECHQHTKCS---WLYTKACAGSSSHWVWVWFLGSLVIYIV 215
DB 142 VCHPVPVGFSSQSSLEFKCYPMWTSCEDEKNULEVLQK---GTSQTVNIVICGLASRMRLALVI 198
OY 216 CSTVGLIIC-----VKK--RKPRGDVVKVIVSVORRROAEAGEATVIALQAPPDVT 266
```

Db 199 PYVMGLITITFEVLYIKVKKRKN--EMLPARADPOQME-----DYPCHNTA 249
 QY 267 VAVEETI 273
 Db 250 APVOETL 256

RESULT 2

B-cell activation protein CD40 precursor - human
 A:Accession: S04460
 A:Reference number: S04460; MUID:89356608
 A:Accession: S04460
 A:Molecule type: mRNA
 A:Residues: 1-277 <STA>
 A:Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor
 A:Reference number: S04460; MUID:89356608
 A:Accession: S04460
 A:Molecule type: mRNA
 A:Residues: 1-277 <STA>
 A:Cross-references: EMBL:60592; NID:929850; PIDN:CAA43045.1; PID:929851
 R:Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
 J. Immunol. 142, 562-567, 1989
 A:Title: Biochemical characteristics and partial amino acid sequence of the receptor-11k
 A:Reference number: A60771; MUID:89093941
 A:Accession: A60771
 A:Molecule type: protein
 A:Residues: 21-50 <BRA>
 A:Experimental source: Burkitt lymphoma cell line Raji
 C:Genetics:
 A:Gene: GDB:CD40
 A:Cross-references: GDB:215268; OMIM:109535

A:Map position: 20q12-20q13.2
 C:Superfamily: CD27 antigen; NGF receptor repeat homology
 C:Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane protein
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-277/Product: B-cell activation protein CD40 #status experimental <MAT>
 F:21-193/Domain: extracellular #status predicted <EXT>
 F:194-215/Domain: transmembrane #status predicted <TM>
 F:216-277/Domain: intracellular #status predicted <CYT>
 F:153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 17.0%; Score 267.5; DB 2; Length 277;
 Best Local Similarity 26.1%; Pred. No. 1.2e-12;
 Matches 71; Conservative 50; Mismatches 116; Indels 35; Gaps 9;

QY 20 VRLVLYLFLGAPCYAPAL-----PSCKEDPYGSECCPKSPGYRVEACGELTGT 74
 Db 1 MRLPLQCVLMG--CLTAVHPRPPACREKQYLINSQCCSLCPQOKLVSDCTETETE 58
 QY 75 CEBCPPGYIAHLNGLSKLQCCOMCDPAMGLRASRNCSTENAVCGSPGHFCIVODG 134
 Db 59 CLPCESEFLDYNRRFTHQHOKYCDPNGLRYQOKGSETDITICERGBHC---TSEA 115
 QY 135 CAACRAVATSSPGQRYQKGTESODTLQCNCPGTFS--FNGTLEBQHQTCSM--LVTK 191
 Db 116 CESCVAHRCSPFGVKQIATGVSDICPCPGVFSNVSSAFAEKHPMTSETKDLVQ 175
 QY 192 AGAGTSSHMVWFLLSGSLVIVVCGTGLICVRRKRGDVAVKVAVORROBAE 251
 Db 176 Q-AGTKTKDVCGPDRLALAVIPIIFGLRA-----ILLVAVIKVAKKPTNK 225
 QY 252 ATVTEALQAPDV-----TTVAVEETI 273
 Db 226 AP--HPKQEPFNFDDLPGSNTAPVQETL 255

RESULT 3
 B43692
 T2 protein - rabbit fibroma virus

C:Species: rabbit fibroma virus, Shope fibroma virus
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C:Accession: B43692
 R:Upton, C.; Delange, A.M.; McFadden, G.
 Virology 160, 20-30, 1987
 A:Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomer
 A:Reference number: A43692; MUID:87321103
 A:Accession: B43692
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-325 <OPT>
 A:Cross-references: GB:M17433
 C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
 F:64-105/Domain: NGF receptor repeat homology <NG2>
 F:106-147/Domain: NGF receptor repeat homology <NG3>

Query Match 16.5%; Score 260; DB 2; Length 325;
 Best Local Similarity 31.5%; Pred. No. 4.8e-12;
 Matches 62; Conservative 25; Mismatches 80; Indels 30; Gaps 8;

QY 20 VRLVLYLFLGAPCYAPALP-----SCKEDPYGSECCPKSPGYRVEACGELTGT 73
 Db 1 MRLPLQCV--VYVGDVPPYSSNCGKCGHDYKDLCCASCHFGFYASRLCGFSWT 59
 QY 74 VCBPCEGYIAHLNGLSKLQCCOMCDPAMG--LRASRNCSTENAVCGSPGHFCIVODG 132
 Db 60 VCBPCEGYIAHLNGLSKLQCCOMCDPAMG--LRASRNCSTENAVCGSPGHFCIVODG 117
 QY 133 DHCACRAVATSSPGQRYQKGTESODTLQCNCPGTFSFN--GTLEEC----- 179
 Db 118 NGCRIC-APQTKCPAGYGSVGHTRAGDTLCEKCPHTYSDSLSPTRCGTFSNYSVGN 176
 QY 180 ---QHQTCSMLVTKAG 193
 Db 177 LYPVNETSCT--TTAG 190

RESULT 4

A33356
 tumor necrosis factor receptor 2 precursor [validated] - human
 N:Alternate names: 75k tumor necrosis factor receptor; TNF receptor type 2
 C:Species: Homo sapiens (man)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 08-Dec-2000
 C:Accession: A33356; A36475; A48416; A36007; A23666; B35010; I38094
 R:Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, Science 248, 1019-1023, 1990
 A:Title: A receptor for tumor necrosis factor defines an unusual family of cellular a
 A:Reference number: A33356; MUID:90260639
 A:Accession: A33356
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-461 <SMI>
 A:Cross-references: GB:M32315; NID:9189185; PIDN:AAA59929.1; PID:9189186
 R:Kohno, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squir Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
 A:Title: A second tumor necrosis factor receptor gene product can shed a naturally oc
 A:Reference number: A36475; MUID:91045591
 A:Accession: A36475
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-195; R', 197-461 <KOH>
 A:Cross-references: GB:M55994; GB:M38549; NID:9339757; PIDN:AAA36755.1; PID:9339758
 R:Demich, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahn, H.W.; Gentz, R.; Brockhaus, Cytokine 2, 231-237, 1990
 A:Title: Two human TNF receptors have similar extracellular, but distinct intracellular
 A:Reference number: A48416; MUID:91370690
 A:Accession: A48416
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 23-461 <DEM>
 A:Cross-references: GB:S63368; NID:9235648; PIDN:AAB19824.1; PID:9235649
 A:Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBI:63371)

OY 178 ECO-----HOTKCSMLVTKAGACTSSSHWVWFLSGSLVIVI 214
 Db 178 YIDVEITLYPVNDTSCTRTT---TGLSES-----ITLSELTITM 214

RESULT 7

gene G4R protein - variola virus
 N:Alternate names: B28R protein (COP)
 C:Species: variola virus
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Mar-2001
 A:Accession: D36858; S46888; S32385; S35987
 R:Blinov, V.M.
 submitted to GenBank, November 1992

A:Reference number: A36859
 A:Accession: D36858
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-349 <BLI>
 A:Cross-references: GB:X69198; NID:g456758; PIDN:CAA49137.1; PID:g457087
 A:Experimental source: strain India-1967, ssp. major, isolate Ind3
 R:Kolykhaylov, A.A.; Blinov, V.M.; Gylorov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; Froi
 submitted to the EMBL Data Library, April 1992
 A:Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H P
 A:Reference number: S46888
 A:Accession: S46888
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-349 <KOL>
 A:Cross-references: EMBL:X67117; NID:g516428; PIDN:CAA47540.1; PID:g516449
 A:Experimental source: strain India-1967, isolate Ind3
 R:Shchelkunov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.
 FEBS Lett. 319, 80-83, 1993
 A:Title: Genes of variola and vaccinia viruses necessary to overcome the host protective
 A:Reference number: S32385; MOID:93202281
 A:Accession: S32385
 A:Molecule type: DNA
 A:Residues: 31-168 <SHC>
 A:Cross-references: EMBL:X69198
 A:Experimental source: strain India-1967, ssp. major
 C:Genetics:
 A:Gene: G4R
 C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
 F:32-66/Domain: NGF receptor repeat homology <NGF>
 F:68-109/Domain: NGF receptor repeat homology <NG2>
 F:110-151/Domain: NGF receptor repeat homology <NG3>

Query Match 16.3%; Score 257; DB 2; Length 349;
 Best local Similarity 29.3%; Pred. No. 8.5e-12;
 Matches 66; Conservative 23; Mismatches 94; Indels 42; Gaps 8;
 OY 21 LRLVLTFLTGAPC-----VAPALPCKEEDYPVGSCECPGSPRYKACGEL 70
 Db 1 MMSVLVLTFLTSCIIINGRDAPYPPNPKCKDTEYKHNHLCCLSCPGTYASRLCDSE 60
 OY 71 TGVVPCPCPGTYIAHLNGLSKCLQCG-MODPAMGLARNSRGTENAVCGGSPGHFCY 129
 Db 61 TINTQCTPCSGTFTSRNNHLPCLSCNGRN--SNOVETSCNTNHRICEGSPGYICLL 118
 OY 130 ODGDHCACRAVATSSPGORVOKGTESODTLQONCPGTF-----PAGTLE 177
 Db 119 KSSGCKACVSGKIGV--SGHVSVDVLCSPGFGYSHITVSADKCEPVPNNITN 177
 OY 178 ECO-----HOTKCSMLVTKAGACTSSSHWVWFLSGSLVIVI 214
 Db 178 YIDVEITLYPVNDTSCTRTT---TGLSES-----ITLSELTITM 214

RESULT 8
 154182
 tumor necrosis factor receptor 2-related protein - human

C:Species: Homo sapiens (man)
 C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
 C:Accession: I54182
 R:Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
 Genomics 16, 214-218, 1993
 A:Title: Construction and evaluation of a hncDNA library of human 12p transcribed seq
 A:Reference number: I54182; MOID:93252381
 A:Accession: I54182
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-435 <RES>
 A:Cross-references: GB:L04270; NID:g339761; PIDN:AAA36757.1; PID:g339762
 C:Genetics:
 A:Gene: GDB:LTBR
 A:Cross-references: GDB:1230195; OMIM:600979
 A:Map position: 12p13.3-12p13.1
 C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match 16.0%; Score 253; DB 2; Length 435;
 Best local Similarity 26.7%; Pred. No. 2e-11;
 Matches 86; Conservative 37; Mismatches 127; Indels 72; Gaps 16;
 OY 4 PG-DWGPPWRSTPRDVLRLVLYTLF-----GAPCYAPALPSCK--EDRY--PVGS 51
 Db 10 PGLAMGP-----LVLGLEGLAASQPAVPPYASNGTCRDQKEYEYEPQHR 56
 OY 52 ECCPKSPGTRYKAEAGELGTGYCEPCPGTYIAHLNGLSKCLQCGMCDPAMGLARSRNC 111
 Db 57 ICCRCPPGTYVASAKSRIRDTVCATCAENSNEHNNYLTICOLCRCPDVMLEBIAC 116
 OY 112 SRLENVCCGSPHFCIVODGHCACRAVATSSPG-----ORVKGGESODTLQONC 165
 Db 117 TSKRKQOCROQPMFCAM-ALECTHCELLSDCPGTEALKEVKGKNNH-----CYPC 170
 OY 166 PEGT-----SPNCTLECOHQTKC-SMLVTKAGACTSSSHWVW-----FLSGSLVI 212
 Db 171 KAGHPONTSSPSA---RCQPHTRCENGLVEAPGTAOSTTCKNPLEPLPPMSGTMLM 227
 OY 213 VIVCSYVGLI-----CYKRRKPRGDVYKIVSVQRKQAEAGATYIEALQAP----- 261
 Db 228 LAVLPLAPFLLATVESCISKSHP--SLCRKLGLILKRPOEGPVPVAGSWEPKAP 285
 OY 262 --PDVTTVAVEETIPSGTGRSP 281
 Db 286 YFPDL-----VQPLRPLISGDVSP 303

RESULT 9
 S12783
 OX40 antigen precursor - rat
 N:Alternate names: nerve growth factor receptor homolog
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
 C:Accession: S12783; S08036
 R:Maliet, S.; Fossum, S.; Barclay, A.N.
 EMBO J. 9, 1063-1068, 1990
 A:Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphoc
 A:Reference number: S12783; MOID:90214614
 A:Accession: S12783
 A:Molecule type: mRNA
 A:Residues: 1-271 <MAL>
 A:Cross-references: EMBL:X17037; NID:g57830; PIDN:CAA34897.1; PID:g57831
 C:Superfamily: CD27 antigen; NGF receptor repeat homology
 C:Keywords: growth factor receptor; transmembrane protein
 F:1-15/Domain: signal sequence #status predicted <Sig>
 F:20-271/Product: OX40 antigen #status predicted <MAT>
 F:211-235/Domain: transmembrane #status predicted <TM>

Query Match 15.2%; Score 240.5; DB 2; Length 271;
 Best local Similarity 34.9%; Pred. No. 1.1e-10;
 Matches 51; Conservative 16; Mismatches 54; Indels 25; Gaps 5;

OY 41 SCKEDYEVPGSECCPKSPGYRVKACGELTGVCEPPTGYIAHLNGLSKLQCCMD 100
 : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
 DB 25 NCVKHTYPSGHHKCCRECPGHHGMSRCDHTRTDTPCHPCETGYNEAVN-YDTCCKQCTQCN 83
 OY 101 PAMGLRASNCRSTENAVCGSPGHFCIVQDGDHCAACRAVATSSPGORVKGTESDPT 160
 : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
 DB 84 HRSGSELKQNCPTEDTDTVQCCRPG--TQPRQDSSH-----KLGVD---- 121
 OY 161 LCQNCPPGTFSPNGTLEECQHOTKCS 186
 : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
 DB 122 -CVPCPPGHFSP-GSNQACKPWTNCT 145

RESULT 10

GOVZML
 T2 protein - myxoma virus (strain Lausanne)
 C:Species: myxoma virus
 C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 18-Jun-1999
 C:Accession: A40566
 R:Upton, C.; Maceo, J.L.; Schreiber, M.; Mcfadden, G.
 Virology 184, 370-382, 1991
 A:Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis factor
 A:Reference number: A40566; MUID:91335768
 A:Accession: A40566
 A:Molecule type: DNA
 A:Residues: 1-326 <UPT>
 A:Cross-references: GB:M95181; GB:M37976; NID:g332309; PIDN:AAA46632.1; PID:g332310
 C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
 C:Keywords: glycoprotein
 F:64-105/Domain: NGF receptor repeat homology <NG2>
 F:106-147/Domain: NGF receptor repeat homology <NG3>
 F:66,181,205,238/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 15.1%; Score 238.5; DB 1; Length 326;
 Best Local Similarity 26.8%; Pred. No. 1.8e-10;
 Matches 73; Conservative 30; Mismatches 104; Indels 65; Gaps 11;

OY 20 VRLVLYLFTL-----GAPCYAPALPSCKEDEYVSGCCPKSPGYRVKACGELTGT 73
 : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
 DB 1 MRLTLALLAYVACVYGGAP-YGADRGRKGRNDYERKDGICTSPGSAVSLCGPSDT 59
 OY 74 VCEPPEPGTYIAHLNGLSKLQCC-MCDPAMGLRASNCRSTENAVCGSPGHFCIVQDG 132
 : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
 DB 60 VCSCKNEFTASTNHAPACVSCGRG--TGHLSQSQSDKTRDRVCDSAGNYLKGQ 117
 OY 133 DHCACRAVATSSPGORVKGTESDPTLQNCPPGTFSPN-GTLEECQ----- 180
 : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
 DB 118 EECRRIC-APKTCRPAIGVSGHTRTGDICTCPRITYSDAVSSTETCTSSFNYSVERN 176
 OY 181 ---HOKCSWLVTAGA-----GTSSHWVWFLSGS 209
 : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
 DB 177 IYVNDTSGT---TTAGDNEVYKTSFSEVTLNHTDCDPVFHTTEYTGSGSEGAGGFTGM 233
 OY 210 ---LVIVYCSVGLITCVKRRKPRGDVVKV 238
 : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
 DB 234 DRYQNTTKMCTLINEIRCE-----GDAVRTI 260

RESULT 11

148700
 gene ox40 protein - mouse
 N:Alternate names: Ox40 antigen
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
 R:Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J.;
 J. Immunol. 151, 5261-5271, 1993
 A:Title: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell int
 A:Reference number: 148700; MUID:94044750
 A:Accession: 148700
 A:Status: translated from GR/EMBL/DBJ

A:Molecule type: mRNA
 A:Residues: 1-272 <RES>
 A:Cross-references: EMBL:Z21674; NID:g312827; PIDN:CAA79772.1; PID:g312828
 R:Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.
 Eur. J. Immunol. 25, 926-930, 1995
 A:Title: Gene structure and chromosomal localization of the mouse homologue of rat OX
 A:Reference number: 148334; MUID:95255413
 A:Accession: 148334
 A:Status: translated from GR/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-14, 'G', 16-272 <RE2>
 A:Cross-references: EMBL:X85214; NID:g732818; PIDN:CAA59476.1; PID:g732819
 C:Genetics:
 A:Gene: ox40
 A:Insertions: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1
 C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 13.7%; Score 215.5; DB 2; Length 272;
 Best Local Similarity 31.5%; Pred. No. 7.5e-09;
 Matches 46; Conservative 17; Mismatches 58; Indels 25; Gaps 5;

OY 41 SCKEDYEVPGSECCPKSPGYRVKACGELTGVCEPPTGYIAHLNGLSKLQCCMD 100
 : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
 DB 26 NCVKHTYPSGHHKCCRECPGHHGMSRCDHTRTDTPCHPCETGYNEAVN-YDTCCKQCTQCN 84
 OY 101 PAMGLRASNCRSTENAVCGSPGHFCIVQDGDHCAACRAVATSSPGORVKGTESDPT 160
 : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
 DB 85 HRSGSELKQNCPTEDTDTVQCCRPG-----TQPRQDSSH-----KLGVD---- 122
 OY 161 LCQNCPPGTFSPNGTLEECQHOTKCS 186
 : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
 DB 123 -CVPCPPGHFSP-GNNQACKPWTNCT 146

RESULT 12

B38634

tumor necrosis factor receptor type 2 precursor - mouse

C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
 C:Accession: B38634; A40254; S54816
 R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen,
 Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
 A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis facto
 A:Reference number: A38634; MUID:91187885
 A:Accession: B38634
 A:Molecule type: mRNA
 A:Residues: 1-474 <LEW>
 A:Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
 R:Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; J
 Mol. Cell. Biol. 11, 3020-3026, 1991
 A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors f
 A:Reference number: A40254; MUID:91246168
 A:Accession: A40254
 A:Molecule type: mRNA
 A:Residues: 1-474 <GOO>
 A:Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
 R:Kisner, M.; Fellous, R.; Feldmann, M.; Chernajovsky, Y.
 Submitted to the EMBL Data Library, May 1995
 A:Description: Characterization of the promoter region of the murine p75-TNF receptor
 A:Reference number: S54816
 A:Accession: S54816
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-22 <KIS>
 A:Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA60618.1; PID:g809044
 C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
 C:Keywords: cytokine receptor; transmembrane protein
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-47/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>
 F:40-77/Domain: NGF receptor repeat homology <NG1>
 F:79-120/Domain: NGF receptor repeat homology <NG2>
 F:166-203/Domain: NGF receptor repeat homology <NG4>

Query Match	13.5%	Score 213.5	DB 2	Length 474
Best Local Similarity	28.5%	Pred. No. 1.7e-08		
Matches	55	Conservative	20	Mismatches 101
				Indels 17
				Gaps

QY	20	VLRVLVLYFLGABCVAPALPSCKEDEY--PVGSE-----	CCPKCSPGYRVKEACGE	69
Db	11	VFEIQLMNLATGHPVPAQVVLPPYRPPEGYECOLISOEYDRKRAKCCAKCPGQVYHFNPK		70
QY	70	LGTGVCEPCPPGPTVIALNLGSKCLOC--QMDPAMGLASRNCSTEAAGCSPGHNC		127
Db	71	TSDFVACADEASMTYQWNOFRTCLSSSCCTTDYETRA---CTIQQRKVCACAGRYC		127
QY	128	IVQ--DGDHCAACRAYATSPGQRVQKGTSEODPTLCNQCPPTFF--PNGLTCECQHQTK		185
Db	128	ALKTHSGSCRQCMRLSKCGGFGFVASSRAPNGNVLCKACAPGTFSDTTSSTVDCRPRIK		187
QY	186	SWLVTKAGAGCTSS	198	
Db	188	SILAIPGNASTDA	200	

RESULT 13
148854
gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C:Accession: 148854
R:Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
Mamm. Genome 5: 726-727, 1994
A:Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
A:Reference number: 148854; MUID:95178848
A:Accession: 148854
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-459 <RES>
A:Cross-references: EMBL:X76401, NID:9433830, PTDN:CA53961.1, PTD:9433831
A:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology <NGF>
A:151-188/Domains: NGF receptor repeat homology <NGF>

	Query Match	13.5%	Score 212.5;	DB 2;	Length 459;
	Best Local Similarity	30.9%;	Pred. NO. 1.ge-08;		
	Matches 46;	Conservative 18;	Mismatches 80;	Indels 5;	Gaps 4;
OY	53 CCPKCSPEGYRKAEAGCELTGTVCECPPTGTIAHLNLSKCLQC - QMCDPAMGLRASRNC	111			
	: : : :				:
Db	39 CCAKCPQGYLKHFNCKTSDTYCADCEASMTYYWNQPRICLSSSSC - STDQVETIRAC	96			
OY	112 SRTENAVCGSPBGEHCIVQ - DGDHCAACRAYATSSPCGRVOKGGTESODTLQCNCPPTG	170			
	::: : : : :: : :				:
Db	97 TKOQRNVCAECABGRFCAIKTHSGSRQCMRLSKGPCGVASSRAPNGVLCRKACAPGT	156			
OY	171 S-PNCTLEEQHQTKCSMLVIKAGAGTS	198			
	: : : : :				
Db	157 SDTMSSTDVCCPHRICSTILAIPIGNASTA	185			

```

RESULT 14
JC2395
Fas antigen precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999
C:Accession: JC2395; PC2246
R:Kimura, K.; Wakatsuki, T.; Yamamoto, M.
Biochem. Biophys. Res. Commun. 198, 666-674, 1994
A:Title: A variant mRNA species encoding a truncated form of Fas antigen in the rat liver
A:Reference number: JC2395; MUID:94128114
A:Accession: JC2395
A:Molecule type: mRNA
A:Residues: 1-324 <K1M>
A:Cross-references: DDBJ:ID26112; NID:9468486; PIDN:BA05108.1; PID:di1005650; PID:9468487

```

A:Experimental source: thymus
A:Accession: PC2246
A:Molecule type: mRNA
A:Residues: 1-62, 'RPT' <K12>
A:Cross-references: DDBJ:D26113; NID:9468488; PIDD:BA05109.1; PID:d1005651; PID:g468
A:Experimental source: liver
C:Genetics:
A:Introns: 62/1
C:Superfamily: NGF receptor repeat homology
C:Keywords: transmembrane protein
F.1-21/Domain: signal sequence #status predicted <SIG>
F.22-324/Product: Fas antigen #status predicted <MNT>
F.44-79/Domain: NGF receptor repeat homology <NGF>
F.81-124/Domain: NGF receptor repeat homology <NG4>
F.171-188/Domain: transmembrane #status predicted <TM4>

[illegible]

RESULT 15

A40036

apoptosis-mediating surface antigen Fas precursor - human

N:Alternate names: surface antigen Apo-1

C:Species: Homo sapiens (man)

C:Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 21-Jul-2000

C:Accession: A40036; S24543; A38142

R:Ritch, N.; Yonehara, S.; Ishii, A.; Yonehara, M.; Mizushima, S.-I.; Sameshima, M.; Itoh

Cell 66, 233-243, 1991

A:Title: The polypeptide encoded by the cDNA for human cell surface antigen Fas can m

A:Reference number: A40036; MUID:91309137

A:Accession: A40036

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-335 <IT0>

A:Cross-references: GB:M67454; NID:g182409; PIDN:AAA63174.1; PID:g182410

R:Krammer, P.H.

submitted to the EMBL Data Library, February 1992

A:Reference number: S24543

A:Accession: S24543

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-335 <KRA>

R:Cross-references: EMBL:X63717; NTD:g28741; PID:g28742

R:Roehm, A.; Behrmann, I.; Pelk, W.; Pawlita, M.; Waier, G.; Klas, C.; Li-weber, M.; R

J. Biol. Chem. 267, 10709-10715, 1992

A:Title: Purification and molecular cloning of the Apo-1 cell surface antigen, a memb

A:Reference number: A38142; MUID:92268122

A:Accession: A38142

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-134,'Q',136-335 <OE>

A:Experimental source: SKW6.4 cells

A:Note: sequence extracted from NCBI backbone (NCBIP:103810)

A:Note: in NCBI backbone the source is designated as mouse

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 24, 2002, 16:22:05 ; Search time 9.87 Seconds
(without alignments)
1051.281 Million cell updates/sec

Title: US-08-741-095B-26
Perfect score: 1578
Sequence: 1 MEPPGDWGPMPWRSTPRTDV.....VTIVAVEETIPSTGRSPNH 283

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues
Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1575	99.8	283	TR14_HUMAN	Q92956 homo sapien
2	276.5	17.5	289	CD40_MOUSE	P27512 homo muscu
3	267.5	17.0	277	CD40_HUMAN	P25942 homo sapien
4	267	16.9	269	CD40_BOVIN	Q28203 bos taurus
5	260	16.5	325	VT2_SEPKA	P25943 shope fibro
6	259	16.4	461	TNR2_HUMAN	P20333 homo sapien
7	257	16.3	349	VC22_VARV	P36941 variola vir
8	253	16.0	435	TNRC_HUMAN	P36941 homo sapien
9	245.5	15.6	415	TNRC_MOUSE	P50284 mus muscu
10	240.5	15.2	271	OX40_RAT	P15725 ratus norv
11	238.5	15.1	326	VT2_MXIVL	P29825 myxoma viru
12	236	15.0	332	FASA_PIG	O77736 sus scrofa
13	215.5	13.7	272	OX40_MOUSE	P47742 mus muscu
14	213.5	13.5	474	TNR2_MOUSE	P25119 mus muscu
15	206.5	13.1	324	FASA_RAT	O63199 ratus norv
16	206.5	13.1	417	WSL1_HUMAN	O93038 h wsl-1 pro
17	206	13.1	335	FASA_HUMAN	P25445 homo sapien
18	205	13.0	327	FASA_MOUSE	P25446 mus muscu
19	203.5	12.9	425	NGFR_RAT	P07174 ratus norv
20	200.5	12.7	323	FASA_BOVIN	P18167 bos taurus
21	198.5	12.6	416	NGFR_CHICK	P18519 gallus gall
22	194.5	12.3	277	OX40_HUMAN	P43489 homo sapien
23	192	12.2	461	TNR1_RAT	P22934 ratus norv
24	190	12.0	427	NGFR_HUMAN	P08138 homo sapien
25	176.5	11.2	256	41BB_MOUSE	P20354 mus muscu
26	172.5	10.9	461	TNR1_PIG	P50555 sus scrofa
27	171.5	10.9	471	TNR1_BOVIN	O19131 bos taurus
28	171	10.8	250	CD27_MOUSE	P41272 mus muscu
29	168.5	10.7	454	TNR1_MOUSE	P25118 mus muscu
30	161	10.2	255	41BB_HUMAN	O07011 homo sapien
31	159	10.1	595	CD50_HUMAN	P28908 homo sapien
32	155	9.8	455	TNR1_HUMAN	P19438 homo sapien
33	148	9.4	260	CD27_HUMAN	P26842 homo sapien

34	143.5	9.1	1786	1	LMB1_HUMAN	P07942 homo sapien
35	139.5	8.8	5376	1	ZAN_MOUSE	O88799 mus muscu
36	133.5	8.5	4393	1	PGM_HUMAN	P98160 homo sapien
37	130.5	8.3	1786	1	LMB1_MOUSE	P02469 mus muscu
38	127.5	8.1	3707	1	PGM_MOUSE	Q05793 mus muscu
39	126	8.0	1557	1	LM1_CAEL	Q18823 caenorhabd
40	126	8.0	1798	1	LM2_HUMAN	P55268 homo sapien
41	125	7.9	722	1	DL1_MOUSE	O61483 mus muscu
42	122	7.7	714	1	DL1_RAT	P97677 ratus norv
43	122	7.7	3106	1	LM2_MOUSE	Q06675 mus muscu
44	121.5	7.7	1964	1	NTC4_MOUSE	P31695 mus muscu
45	121	7.7	755	1	COMP_RAT	P35444 ratus norv

ALIGNMENTS

```

RESULT 1
ID      TR14_HUMAN
AC      Q92956; Q90M65;
DT      20-AUG-2001 (Rel. 40, Created)
DR      20-AUG-2001 (Rel. 40, Last sequence update)
DE      TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 14 PRECURSOR
DE      (HERPESVIRUS ENTRY MEDIATOR) (TUMOR NECROSIS FACTOR RECEPTOR-LIKE 2)
GN      TNFRSF14 OR HWEM.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Cervix adenocarcinoma;
RX      MEDLINE=97053782; PubMed=8898196;
RA      Montgomery R.I., Warner M.S., Lum B.J., Spear P.G.;
RT      "Herpes simplex virus-1 entry into cells mediated by a novel member of
RT      the TNF/NGF receptor family.";
RL      Cell 87:427-436(1996).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=97306336; PubMed=9162061;
RA      Kwon B.S., Tan K.B., Ni J., Oh K.-O., Lee Z.H., Kim K.K., Kim Y.-J.,
RA      Wang S., Gentz R., Yu G.-L., Harrop J., Lyn S.D., Silverman C.,
RA      Porter T.G., Truneh A., Young P.R.;
RT      "A newly identified member of the tumor necrosis factor receptor
RT      superfamily with a wide tissue distribution and involvement in
RT      lymphocyte activation.";
RL      J. Biol. Chem. 272:14272-14276(1997).
RN      [3]
RP      SEQUENCE FROM N.A.
RA      Zhang W., Wan T., Cao X.;
RT      Submitted (MAY-1999) to the EMBL/Genbank/DBJ databases.
-!- FUNCTION: RECEPTOR FOR TNFSF14. INVOLVED IN LYMPHOCYTE ACTIVATION.
PLAYS AN IMPORTANT ROLE IN HSV PATHOGENESIS BECAUSE IT ENHANCED
THE ENTRY OF SEVERAL WILDTYPE HSV STRAINS OR BOTH SEROTYPES INTO
CHO CELLS, AND MEDIATED HSV ENTRY INTO ACTIVATED HUMAN T CELLS.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (PROBABILE).
-!- TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH THE HIGHEST EXPRESSION
IN LUNG, SPLEEN, AND THYMUS.
-!- SIMILARITY: CONTAINS 1 LA-NGR/TNFR-TYPE CYSTEINE-RICH REGION.
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EMBL: U70321; AAB58354.1; -
DR      EMBL; U81232; AAD0505.1; -

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DR EMBL: AF153978; AAF75588.1; -
DR HSSP: P25942; 1CDF.
DR MIM: 602746; -
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 3.
DR ProDom: PD000771; TNFR_c6; 1.
DR SMART: SM00208; TNFR_3.
DR PROSITE: PS00652; TNFR_NGFR_1; 1.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
KM Receptor: Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 38
FT CHAIN 39 283
FT
FT DOMAIN 39 202
FT TRANSMEM 203 223
FT DOMAIN 224 283
FT
FT DOMAIN 42 162
FT
FT REPEAT 42 75
FT REPEAT 78 119
FT REPEAT 121 162
FT DISULFID 42 53
FT DISULFID 54 67
FT DISULFID 57 75
FT DISULFID 78 93
FT DISULFID 96 111
FT DISULFID 121 127
FT DISULFID 138 162
FT CARBOHYD 110 162
FT CARBOHYD 173 173
FT CONFLICT 17 17
SQ SEQUENCE 283 AA; 30392 MW; 46CE13C2C7024ZC1 CRC64;

Query Match 99.88; Score 1575; DB 1; Length 283;
Best local Similarity 99.68; Pred. No. 5e-120;
Matches 282; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 MEPPGMGPMPSPRSTPTDYLRLVLTFLGACVAPALPSCKEDEPVSECCPKSPG 60
DB 1 MEPPGMGPMPSPRSTPTDYLRLVLTFLGACVAPALPSCKEDEPVSECCPKSPG 60
OY 61 YRKVEAGELGTVCCEPPTGYIAHLNGLSKLQCCMDPAGLRASRNCSTENAVCG 120
DB 61 YRKVEAGELGTVCCEPPTGYIAHLNGLSKLQCCMDPAGLRASRNCSTENAVCG 120
OY 121 CSGGHFCIYODGDHCAACRAVATSSPGQRYQKGTESDPTLCONCPPTGTPNGTLEECQ 180
DB 121 CSGGHFCIYODGDHCAACRAVATSSPGQRYQKGTESDPTLCONCPPTGTPNGTLEECQ 180
OY 181 HOKKCSMLVTKAGAGTSSSHWMMPLSGSLVYIVGCVSTVGLLVCVRRKRGDVAVIYS 240
DB 181 HOKKCSMLVTKAGAGTSSSHWMMPLSGSLVYIVGCVSTVGLLVCVRRKRGDVAVIYS 240
OY 241 YOKKROEAGEATVIALQAPPDVTVAVETIIPSTGSRPNH 283
DB 241 YOKKROEAGEATVIALQAPPDVTVAVETIIPSTGSRPNH 283
RESULT 2
CD40_MOUSE STANDARD; PRT: 289 AA.
AC P27512;
DT 01-AUG-1992 (rel. 23, Created)
DT 01-OCT-1996 (rel. 34, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDM40).
GN TNFRSF5 OR CD40.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=92105763; Pubmed=1370315;
RA Torres R.M., Clark E.A.;
RT "Differential increase of an alternatively polyadenylated mRNA
species of murine CD40 upon B lymphocyte activation."
RL J. Immunol. 148:620-626(1992).
RN [2]
RP REVISIONS.
RC STRAIN-BALB/C;
RA Torres R.M.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE=Liver;
RX MEDLINE=93094586; Pubmed=1281194;
RA Grimaldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A.,
RA Howard M., Cockayne D.A.;
RT "Genomic structure and chromosomal mapping of the murine CD40 gene."
RL J. Immunol. 149:3921-3926(1992).
CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL: M83312; AAB08705.1; -
DR EMBL: M84126; AAA37404.1; -
DR EMBL: M94129; AAA37404.1; JOINED.
DR EMBL: M94128; AAA37404.1; JOINED.
DR EMBL: M94127; AAA37404.1; JOINED.
DR PIR: A46476; A46476.
DR HSSP: P25942; 1CDF.
DR MGD: MGI:88336; Trif55.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 4.
DR ProDom: PD000771; TNFR_c6; 1.
DR SMART: SM00208; TNFR_3.
DR PROSITE: PS00652; TNFR_NGFR_1; 1.
DR PROSITE: PS50050; TNFR_NGFR_2; 4.
KM Receptor: B-cell; Glycoprotein; Transmembrane; Repeat; Signal.
FT SIGNAL 1 19
FT CHAIN 20 289
FT DOMAIN 20 193
FT TRANSMEM 194 215
FT DOMAIN 216 289
FT
FT DOMAIN 25 187
FT REPEAT 25 60
FT REPEAT 61 103
FT REPEAT 104 144
FT REPEAT 145 187
FT CARBOHYD 153 153
SQ SEQUENCE 289 AA; 32111 MW; C791CB6D2FEA574E CRC64;

Query Match 17.5%; Score 276.5; DB 1; Length 289;
Best local Similarity 27.9%; Pred. No. 1.9e-15;
Matches 69; Conservative 43; Mismatches 106; Indels 29; Gaps 8;
OY 41 SCKEDEVPSSECCPKSPGKYRKVEAGELGTVCCEPPTGYIAHLNGLSKLQCCMD 100
DB 25 TCSDKQYLHDGQCDCDCCPGRSLTSHCTALEKQCHPCDSGERSAQMNEIRCHQRHCE 84
OY 101 PAMGLASRNCSTENAVAGCCSGHFCIYODGDHCAACRAVATSSPGQRYQKGTSSDPT 160
DB 85 PNOGLVKKRKGTAESPTVCKCKEGHCTSKD---CECAQHPPCIPFGVMEATETPTDT 141
OY 161 LCQNCPPGTGTPNGTL-EECQHGTCKS---MLVTKAGAGTSSSHWMMPLSGSLVYIV 215


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CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U5745; AAC48710.1; -.
CC HSSP: P25942; 1CDF.
CC InterPro: IPR001368; TNFR_c6.
CC Pfam: PF00020; TNFR_c6; 4.
CC ProDom: PD000771; TNFR_c6; 1.
CC SMART: SM00208; TNFR_4.
CC PROSITE: PS00652; TNFR_NGFR_1; 1.
CC PROSITE: PS00500; TNFR_NGFR_2; 1.
CC Receptor: B-cell; Glycoprotein; Transmembrane; Repeat; Signal.
CC SIGNAL 1 19
CC CHAIN 20 >269
CC DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 194 215 POTENTIAL.
CC DOMAIN 216 >269 CYTOPLASMIC (POTENTIAL).
CC DOMAIN 25 187 4 X TNFR-CYS.
CC REPEAT 61 103 TNFR-CYS 1.
CC REPEAT 104 144 TNFR-CYS 2.
CC REPEAT 145 187 TNFR-CYS 3.
CC CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC NON_TER 269 269
CC SEQUENCE 269 AA; 29983 MW; 74690330F95F387 CRC64;

Query Match 16.9%; Score 267; DB 1; Length 269;
Best local Similarity 28.0%; Pred. No. 1e-14;
Matches 65; Conservative 43; Mismatches 110; Indels 14; Gaps 5;

QY 20 VLRVLYLFLFLG---APCYAPALPSCKEDEYPVGSCECPSPGYRKEAGELTGTVE 76
DB 1 MVRLLPQCLEFWGFFLVAHVSEPAFACGEKQYPVNSLCCDLCPPGOKLVNDCTEVSKTECQ 60
QY 77 PCBPGRVIAHLNLSKLCQCOMCDPAMGLRASNCRSTENAVGCCSGHRCIYODDGHCA 136
DB 61 SCCKGEFLSTWNEKCYCHEHRCNPMLGLRQSEGTLNLTDTICVCGEGHC---TSHTCE 117
QY 137 ACRAVATSSPGQVRQVKGTESDTLCONCPPTGFS--PNGTLEECOHQTKCSWL-VTKAGA 194
DB 118 SCTPHSLCLPBGFEVKQIANGLDLTVECPDLGPFNSVSAFECHEMTSECRKGLVEQHV 177
QY 195 GSSSSMMWMMFLSGSLVIYIVCTVGLIICVKKRPRGDVYKVIYSVQKRQ 246
DB 178 GINKTDVVGCFQSRMRTLVIVPTMGVLFVALL-----VSACIRNITKRQ 223

RESULT 5
VT2_SFVKA STANDARD; PRT; 325 AA.
ID VT2_SFVKA
AC P25943;
DT 01-MAY-1992 (rel. 22, Created)
DT 01-MAY-1992 (rel. 22, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
GN T2.
OS Shope fibroma virus (strain Kasza) (SFV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Leporipoxvirus.
OX NCBI_TaxID=10272;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87321103; PubMed=2820128;

```

```

RA Upton C., Delange A.M., McFadden G.;
RT "Tumorigenic poxviruses: genomic organization and DNA sequence of the
RL telomeric region of the Shope fibroma virus genome.";
RL Virology 160:20-30(1987).
RN [2]
RP FUNCTION.
RX MEDLINE=91207415; PubMed=1850261;
RA Smith C.A., Davis T., Mignall J.M., Din W.S., Farrah T., Upton C.,
RA McFadden G., Goodwin R.G.;
RT "2 open reading frame from the Shope fibroma virus encodes a soluble
RL form of the TNF receptor.";
RL Biochem. Biophys. Res. Commun. 176:335-342(1991).
CC -1- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
CC REACH CELLULAR TARGET AND THEREBY DEAMPENING THE POTENTIAL
CC ANTI-VIRAL EFFECTS OF THE CYTOKINE.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M17433; -. NOT ANNOTATED_CDS.
CC PIR: A23727; CA01687.1; -.
CC PIR: B43692; B43692.
CC HSSP: P19438; 1TNR.
CC InterPro: IPR001368; TNFR_c6.
CC Pfam: PF00020; TNFR_c6; 2.
CC ProDom: PD000771; TNFR_c6; 1.
CC SMART: SM00208; TNFR_3.
CC PROSITE: PS00652; TNFR_NGFR_1; 2.
CC PROSITE: PS00500; TNFR_NGFR_2; 1.
CC Receptor: Glycoprotein; Repeat; Signal.
CC SIGNAL 1 16
CC CHAIN 17 325
CC DOMAIN 27 186 4 X TNFR-CYS.
CC REPEAT 27 62 TNFR-CYS 1.
CC REPEAT 63 104 TNFR-CYS 2.
CC REPEAT 105 147 TNFR-CYS 3.
CC REPEAT 148 186 TNFR-CYS 4.
CC CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 325 AA; 35132 MW; 810530339198A71E CRC64;

Query Match 16.5%; Score 260; DB 1; Length 325;
Best local Similarity 31.5%; Pred. No. 4.5e-14;
Matches 62; Conservative 25; Mismatches 80; Indels 30; Gaps 8;

QY 20 VLRVLYLFLFLGAPCYAPALP-----SCKEDYYPVGSCECPSPGYRKEAGELTGT 73
DB 1 MRLIALLVGV-VYYVGDVYPSSNOGCGGHYERKDLCCACGJHGFASRLCGGSGMT 59
QY 74 VCEPCPPGTYIAHLNLSKLCQCOMCDPAMG-LRASNCRSTENAVGCCSPGHFCTYODG 132
DB 60 VCSPECEGFTASTNHPACVSCR--GPCGHLSGSDPCDRTHDRCNCSGTGYCLLKG 117
QY 133 DHCAARAVATSSPGQVRQVKGTESDTLCONCPPTGFSN-GTLEEC----- 179
DB 118 NGCRIC-APQTKPACGVSGHTRADTLCEKCPHTYSDSLSPTEKGTSENVISVGFN 176
QY 180 ---QHOKCSWLVTKAG 193
DB 177 LYPVNETSCT---TTAG 190

RESULT 6
TNR2_HUMAN

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ID TNF2_HUMAN STANDARD: PRT; 461 AA.
AC P20333;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR
GN BINDING PROTEIN 2) (TNF1) (P80) (TNF-R2) (P75) (CD120b) (ETANERCEPT).
DN TNF2_HUMAN OR TNF2_HUMAN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90260639; PubMed=2160731;
RA Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,
RA Dower S.K., Cosman D., Goodwin R.G.,
RT "A receptor for tumor necrosis factor defines an unusual family of
RT cellular and viral proteins.";
RL Science 248:1019-1023(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91045991; PubMed=2172983;
RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,
RA Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.,
RT "A second tumor necrosis factor receptor gene product can shed a
RT naturally occurring tumor necrosis factor inhibitor.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96299745; PubMed=8661109;
RA Beltinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,
RA Lepeslier D., Stallard B.J., Goeddel D.V., Desauvage F.J.,
RA Brodeur G.M.,
RT "Physical mapping and genomic structure of the human TNFR2 gene.";
RL Genomics 35:94-100(1996).
RN [4]
RP SEQUENCE OF 116-461 FROM N.A. AND PARTIAL SEQUENCE.
RX MEDLINE=90349572; PubMed=2166946;
RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,
RA Ringold G.M.,
RT "Complementary DNA cloning of a receptor for tumor necrosis factor
RT and demonstration of a shed form of the receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).
RN [5]
RP SEQUENCE OF 27-31.
RX MEDLINE=90110215; PubMed=2153136;
RA Engelmann H., Novick D., Wallach D.,
RT "Two tumor necrosis factor-binding proteins purified from human
RT urine. Evidence for immunological cross-reactivity with cell surface
RT tumor necrosis factor receptors.";
RL J. Biol. Chem. 265:1531-1536(1990).
RN [6]
RP SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.
RX MEDLINE=91050648; PubMed=2173696;
RA Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,
RA Brockhaus M.,
RT "Purification and partial amino acid sequence analysis of two
RT distinct tumor necrosis factor receptors from HL60 cells.";
RL J. Biol. Chem. 265:20131-20138(1990).
RN [7]
RP CHARACTERIZATION.
RX MEDLINE=93016040; PubMed=1328224;
RA Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,
RA Lipari M.T., Goeddel D.V.,
RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor.
RT Characterization of ligand binding, internalization, and receptor
RT phosphorylation.";
RL J. Biol. Chem. 267:21172-21178(1992).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN TRAF2 COMPLEX.
RX MEDLINE=99221490; PubMed=10206649;
RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;

RT "Structural basis for self-association and receptor recognition of
RT human TRAF2.";
RL Nature 398:533-538(1999).
CC -!- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNF-ALPHA AND
CC APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW
CC LEVEL ON THREONINE RESIDUES.
CC -!- PHARMACEUTICAL: AVAILABLE UNDER THE NAME ENBREL (IMMUNEX AND
CC WYETH-AVERTIS). USED TO TREAT MODERATE TO SEVERE RHEUMATOID
CC ARTHRITIS (RA). ENBREL CONSIST OF THE EXTRACELLULAR LIGAND-BINDING
CC PORTION OF TNFR2 LINKED TO AN IMMUGLOBULIN FC CHAIN. IT BINDS TO
CC TNF-ALPHA AND BLOCKS ITS INTERACTIONS WITH RECEPTORS.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD120b entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd120b.htm"
CC -!- DATABASE: NAME=Enbrel; NOTE=Clinical information on Enbrel;
CC WWW="http://www.enbrelinfo.com/".
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: M32315; AAA59929.1; -;
DR EMBL: M35857; AAA63262.1; -;
DR EMBL: U52165; AAC50622.1; -;
DR EMBL: U52156; AAC50622.1; JOINED.
DR EMBL: U52157; AAC50622.1; JOINED.
DR EMBL: U52158; AAC50622.1; JOINED.
DR EMBL: U52159; AAC50622.1; JOINED.
DR EMBL: U52160; AAC50622.1; JOINED.
DR EMBL: U52161; AAC50622.1; JOINED.
DR EMBL: U52162; AAC50622.1; JOINED.
DR EMBL: U52163; AAC50622.1; JOINED.
DR EMBL: U52164; AAC50622.1; JOINED.
DR EMBL: M55994; AAA36755.1; -;
DR PIR: A35356; A35356.
DR PIR: A36007; A36007.
DR PIR: A36475; A36475.
DR PIR: B35010; B35010.
DR PIR: A23666; A23666.
DR PDB: 1CA9; 12-APR-99.
DR MIM: 191191; -;
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 4.
DR ProDom: PD000771; TNFR_c6; 1.
DR SMART: SMO0208; TNFR_4.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR Receptor: PS50050; TNFR_NGFR_2; 4.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal;
KW Phosphorylation; Pharmaceutical; 3D-structure.
FT SIGNAL 1 22
FT CHAIN 23 461 TUMOR NECROSIS FACTOR RECEPTOR 2.
FT DOMAIN 23 257 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 258 287 POTENTIAL.
FT DOMAIN 288 461 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 39 201 4 X TNFR-CYS.
FT REPEAT 39 76 TNFR-CYS 1.
FT REPEAT 77 118 TNFR-CYS 2.
FT REPEAT 119 162 TNFR-CYS 3.
FT REPEAT 163 201 TNFR-CYS 4.
FT DISULFID 40 53 BY SIMILARITY.
FT DISULFID 54 67 BY SIMILARITY.
FT DISULFID 57 75 BY SIMILARITY.
FT DISULFID 78 93 BY SIMILARITY.
FT DISULFID 96 110 BY SIMILARITY.
FT DISULFID 100 118 BY SIMILARITY.
FT DISULFID 120 126 BY SIMILARITY.
FT DISULFID 134 143 BY SIMILARITY.

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FT FT DISULFID 137 161 BY SIMILARITY.
FT FT DISULFID 164 179 BY SIMILARITY.
FT FT CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 193 193 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CONFLICT 141 141 R -> P (IN REF. 4).
FT FT CONFLICT 196 196 R -> M (IN REF. 1 AND 3).
FT FT CONFLICT 363 363 A -> T (IN REF. 4).
SQ SEQUENCE 461 AA; 48316 MW; 603B50ECD67636F CRC64;

Query Match 16.4%; Score 259; DB 1; Length 461;
Best Local Similarity 32.8%; Pred. No. 7.5e-14;
Matches 59; Conservative 23; Mismatches 76; Indels 22; Gaps 6;

OY 35 YAPALPIS-CKDEBY--PVGSECCPKSPGPRYKKEAGELTGYCECPGPGTYIAHLNGIS 91
Db 32 VAPPESTCRLEBYVDQTAOMCCSKSPQAHKVFCTKTSIDYVCSCEDESTYTQLMNWP 91
OY 92 KCLQCCMPDPAAGLGRASRN-----CSFRFNNAVCGSPGPFCTIVODGDHCAACRAVATSS 145
Db 92 ECLSC-----GSRSSDQVETQACTRQGNICTCRPMYCALSKSQECCRLCAPLRKR 144
OY 146 PCQRYOKGTEBQDTLCQNCPPGTS-PNGTLEECOHQTKCSMLVTKAGAG-----TSSS 199
Db 145 PCGVGARPETETSDVVCPCAPGTFSMTSLSDICRPHQICNVVAIPGNASDAVACTSTS 204

RESULT 7
VC22_VARY STANDARD; PRT; 349 AA.
AC P34015;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE PROTEIN C22/B28 HOMOLOG.
GN GAR.
OS Variola virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10255;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=INDIA-1967 / ISOLATE IND3;
RX MEDLINE=93202281; PubMed=8384129;
RA Shchelkunov S.N., Bilnov V.M., Sandakhchiev L.S.;
RT "Genes of variola and vaccinia viruses necessary to overcome the host
RT protective mechanisms."
RL FEBS Lett. 319:80-83(1993).
CC -I- SIMILARITY: CONTAINS 2 LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGIONS.
CC CC
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CC -----
CC DR EMBL; X69198; CAA49137.1; -.
CC DR EMBL; X67117; CAA47540.1; -.
CC DR PIR; D36858; D36858.
CC DR PIR; S35987; S35987.
CC DR PIR; S46888; S46888.
CC DR HSSP; P19438; 1NCF.
CC DR InterPro; IPR001368; TNFR_c6.
CC DR Pfam; PF00020; TNFR_c6; 2.
CC DR ProDom; PD000771; TNFR_c6; 1.
CC DR SMART; SM00087; TNFR_2.
CC DR PROSITE; PS00652; TNFR_NGFR_1; 2.
CC DR PROSITE; PS00500; TNFR_NGFR_2; 2.
CC Repeat.
KW DOMAIN 31 108 2 x TNFR-CYS.
FT REPEAT 31 66 TNFR-CYS 1.

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FT REPEAT 67 108 TNFR-C1S 2
SQ SEQUENCE 349 AA: 38189 MW: D45D40B5C6E780EF CRC64:

Query Match 16.3%; Score 257; DB 1; Length 349;
Best Local Similarity 29.3%; Pred. No. 8,4e-14;
Matches 66; Conservative 23; Mismatches 94; Indels 42; Gaps 8;

OY 21 LRLVLYLFLGAPC-----YAPALPSCKEDEVYSGCCPKSGPYRVKACGEL 70
DB 1 MRSVLYLYLFLSCIIINGRDAPAPTPPENGCKDTFYRHHMLCCLSCPGPYVASRLDSK 60
OY 71 TGTVEPCDPGGYIHLNGLSKLCLOCO-MCPDAMGLRASRNCSTRFNAYGCCSPGHFCIV 129
DB 61 TTTQCTPCGSGFTFSRRNHHLPACISCMGRCN--SNQVETRSCNTTHNRICCSPGYICLL 118
OY 130 QGDGDHCAACRAVATSSPGQRYQKGTSTQDPLCONCPGTFSS-----PNCGLE 177
DB 119 KSSSGCKACVSGTKCGIGYGV-SGHTSYGVDIYCSPCGCGYSHRVSSADKCEPVPNNTFN 177
OY 178 EQQ-----HOTKCSMLVTRKAGAGTSSSHWMMFLSGSLVIYI 214
DB 178 YIDVEITLYPVNDTISCTRTT--TGISES-----ILTSELTITM 214

RESULT 8
ID TNRC_HUMAN STANDARD: PRT: 435 AA.
AC P36941.
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE LYMPHOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR
DE 2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR).
GN LTRR OR TNFR OR TNFRSP3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver.
RX MEDLINE=93252381; PubMed=8486360.
RA Baens M., Charifnet M., Cassiman J.J., den Berghe H., Marynen P.;
RA "Construction and evaluation of a hncDNA library of human 12p
RA transcribed sequences derived from a somatic cell hybrid".;
RN Genomics 16:214-218(1993).
RL [2]
RP FUNCTION.
RX MEDLINE=94225209; PubMed=8171323;
RA Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C.,
RA Ehrenfelds B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
RA "A lymphotoxin-beta-specific receptor".;
RL Science 264:707-710(1994).
CC -i- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
CC IMMUNE DEVELOPMENT.
CC -i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -i- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -----
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CC -----
DR EMBL: L04270; AAA36757.1; -
DR HSP: P25942; ICDF.
DR MIM: 600979; -
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF000020; TNFR_c6; 4.
DR ProDom: PD000721; TNFR_c6; 1.

```

DR SMART; SM00208; TNR; 4.
 DR PROSITE; PS00652; TNR_NGFR_1; 2.
 DR PROSITE; PS00652; TNR_NGFR_2; 3.
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 30
 FT CHAIN 31 435
 FT DOMAIN 31 227
 FT TRANSMEM 228 248
 FT DOMAIN 249 435
 FT DOMAIN 42 211
 FT REPEAT 42 81
 FT REPEAT 82 124
 FT REPEAT 125 168
 FT REPEAT 169 211
 FT DISULFID 43 58
 FT DISULFID 59 72
 FT DISULFID 62 80
 FT DISULFID 83 98
 FT DISULFID 101 116
 FT DISULFID 104 124
 FT DISULFID 126 132
 FT DISULFID 139 148
 FT DISULFID 142 167
 FT DISULFID 170 185
 FT CARBOHYD 40 40
 FT CARBOHYD 177 177
 SO SEQUENCE 435 AA; 46709 MW; 624626E022E5656F CRC64;

Query Match 16.0%; Score 253; DB 1; Length 435;
 Best Local Similarity 26.7%; Pred. No. 2.2e-13;
 Matches 86; Conservative 37; Mismatches 127; Indels 72; Gaps 16;

OY 4 PG-DWGPWPWPRTPTDVLRLVLTFL-----GACPYALALSCK--EEY--PVGS 51
 DB 10 PELAGP-----LVLGLEGLLAASQPAVPPYASENQCROEKEYEPEOHR 56
 OY 52 EECPCPKSPGYRKEACGELGTGCEPCPGYIHALNGLSKLOCOMDPMGLASRNC 111
 DB 57 ICCSKCPPTGYSAKCSRIKDYCATCAENSNEMNWLITCOLCPDPPVGLLEIAPC 116
 OY 112 SRTENAVGCGSPGHFCIVODGDHCAACRAVATSPG-----QRYQKGTESQDTLCONC 165
 DB 117 TSKRKTCRCQCGMFCAM-ALECHCELLSPCPTGEALKEDEYKGNH-----CYPC 170
 OY 166 PPGTF-----SPMGTEECOHQK-C-SLVYTRAGACTSSSHVWVW-----FLSGSLVI 212
 DB 171 KAGHPOMTSSPSA---RCOPHTRCENOGIVEAAPTASDITCKNPLEPLPEMGTMLM 227
 OY 213 VIVCGTVGLI-----CVKRRKRGDVVYKIVSVORROEAGEATVTEALAP----- 261
 DB 228 LAVLLPLAFILLATLVFSCIMKSHP--SLCKRLGSLKRRPOGEGPNPVAGWEPKAPH 285
 OY 262 --PDVTVAVETIPSTGRSP 281
 DB 286 YPPDL---VQPLPLTSGVSP 303
 RESULT 9
 TNR_MOUSE STANDARD; PRT; 415 AA.
 AC P50284;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE LYMPHOTOXIN-BETA RECEPTOR PRECURSOR.
 GN LTRK OR TNR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-CVB; TISSUE-Lung;
 RX MEDLINE=96072804; PubMed=7594541;
 RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
 RA Browning J.L., Ware C.F.;
 RT "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
 and expression.";
 RL J. Immunol. 155:5280-5288(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96163885; PubMed=8586432;
 RA Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
 RA Honjo T.;
 RT "The murine lymphotoxin-beta receptor cDNA: isolation by the signal
 sequence trap and chromosomal mapping.";
 RL Genomics 30:312-319(1995).
 CC -1- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
 IMMUNE DEVELOPMENT.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNR-TYPE CYSTEINE-RICH REGION.
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Query Match 15.6%; Score 245.5; DB 1; Length 415;
 Best Local Similarity 25.9%; Pred. No. 8.3e-13;
 Matches 83; Conservative 40; Mismatches 115; Indels 83; Gaps 15;
 OY 7 WGP-----FPWRSTPTDVLRLVLTFLGACPYALALSCKDEY-- 47
 DB 14 WGPLLIGSLGLVASQPAVPPYRIENQ-----CWD-----QDKEYE 52

FT REPEAT 27 62 TNFR-CYS 1.
 FT REPEAT 63 104 TNFR-CYS 2.
 FT REPEAT 105 147 TNFR-CYS 3.
 FT REPEAT 148 186 TNFR-CYS 4.
 FT CAROHD 66 66 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 326 AA: 35208 MW: ABBF027E947292FF CRC64;

Query Match 15.1%; Score 238.5; DB 1; Length 326;
 Best Local Similarity 26.8%; Pred. No. 2.4e-12;
 Matches 73; Conservative 30; Mismatches 104; Indels 65; Gaps 11;

QY 20 VLRLVLYLFL-----GAPCTAPALPSCKEDEYPVSGCCPKCSGYVKEAGELTGT 73
 DB 1 MRLTLTLLAVYACVYGGGAP-YGADRGKCRGNDYERKDGICTSCPPGSYASRLCGFSGDT 59
 QY 74 VCEPCPGTYIAHLNGLSKLCOQ--MCDPAMGLRASRNCSTRENNVCGSPGHFCIVODG 132
 DB 60 VCSPCNNEFTSTNHAPPCVSCRGRC--TGHLSQSCDKTRDVCDSAGNYCLLKGQ 117
 QY 133 DHCAACRAVATSSPGQVQKGTESQDILCONCPGTESPN-GTLEECQ----- 180
 DB 118 ECGRIC-AKTKCPAGYVSGHTRTGDVLCIKCPRTYSDAVSFTCTSSFNYSVEFN 176
 QY 181 ----HOTKCSMLVTAGA-----GTSSSHWMMFLSGS 209
 DB 177 LYPVNDTSC---TTAGPNEVVKTSFSESVTLNHTDCDPVFHTEYGTSGSEAGGFETDM 233
 QY 210 ---LVYIVCSVGLLICVKKRRKPRGDYVKVI 238
 DB 234 DRYQNTTKMCTNIETRCVE-----GDAVRTI 260

RESULT 12
 ID FASA_PIG STANDARD: PRT: 332 AA.
 AC 07736;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
 DE (APO-1 ANTIGEN) (CD95).
 GN TNFRSF6 OR APR1 OR FAS.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;
 RT "Expression of apoptosis-associated genes in hibernating and stunned
 myocardium of pig";
 RL submitted (Jan-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE
 ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED
 RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING
 SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC
 ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF
 CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING
 APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
 INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
 SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
 AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC
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DR EMBL: AJ001202; CA04596.1;
 DR InterPro: IPR000488; Death.
 DR InterPro: IPR001368; TNFR-C6.
 DR Pfam: PF00531; death; 1.
 DR Pfam: PF00020; TNFR-C6; 3.
 DR SMART: SM00005; DEATH; 1.
 DR SMART: SM00208; TNFR; 3.
 DR PROSITE: PS00652; TNFR_NGFR.2; 2.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 KW Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal.
 FT SIGNAL 1 16 POTENTIAL.
 FT CHAIN 17 332 FASL RECEPTOR.
 FT DOMAIN 17 175 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 176 192 POTENTIAL.
 FT DOMAIN 193 332 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 45 164 3 X TNFR-CYS.
 FT REPEAT 45 81 TNFR-CYS 1.
 FT REPEAT 82 125 TNFR-CYS 2.
 FT REPEAT 126 164 TNFR-CYS 3.
 FT DOMAIN 227 311 DEATH.
 FT CAROHD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 116 116 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 332 AA: 37592 MW: 58803682756BF1B CRC64;

Query Match 15.0%; Score 236; DB 1; Length 332;
 Best Local Similarity 27.5%; Pred. No. 3.9e-12;
 Matches 65; Conservative 30; Mismatches 95; Indels 46; Gaps 9;

QY 42 CKEDXPVSGCCPKCSPPRYRVEKAGELTGT-VCEPCPG-TYIAHLNGLSKLCOQMC 99
 DB 46 CPEGGHREGQFCQCPPEKRRHADTSPGAPQCPGSEGEDYDKNHSSKCRRCVC 105
 QY 100 DPAMGLRASRNCSTRENNVCGSPGHFCIVODGDHCAACRAVATSSPGQVQKGTESOD 159
 DB 106 DEHGIEVKNCTRTQNTCKRCKPNFCHTSCQCHCNPC----- 144
 QY 160 TLQCONCPGTESPNGLTECC--QHOTKCSMLVTAKAGAGSSSHWMMFLSGSLVIYVCS 217
 DB 145 TTCE-----HGVIENCTPTSNTRCREVQSAGS-RSNLHWLM---ALLILIPVA 190
 QY 218 TVGLIICVRRKPRGDYVKVIYVQKRRQEAEGEATVIALOAPDVTVAVEETI 273
 DB 191 LVREYKRRCKRCKENGCKPITS-----NAE-EVPMKIDVLDGKIYTRIAQMKI 239

RESULT 13
 ID OX40_MOUSE STANDARD: PRT: 272 AA.
 AC P47741.
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE OX40L RECEPTOR PRECURSOR (OX40 ANTIGEN).
 GN TNFRSF4 OR TXGP1 OR OX40.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BAIB/C.
 RX MEDLINE=94044750; PubMed=8228223;
 RA Calderhead D.M., Buhlmann J.E., van den Bortwegh A.J.,
 RA Claassen E., Noelle R.J., Fell H.;
 RT "Cloning of mouse OX40: a T cell activation marker that may mediate

RT T-B cell interactions.;

RL J. Immunol. 151:5261-5271(1993).

RN [2]

RX SEQUENCE FROM N.A.

RA Birreland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A., Barclay A.N.;

RT "Gene structure and chromosomal localization of the mouse homologue of rat OX40 protein".

CC Eur. J. Immunol. 25:926-930(1995).

CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

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CC

DR EMBL: Z31674; CAA79772.1; -

DR EMBL: X85214; CAA59476.1; -

DR HSSP: P25942; ICDP.

DR MGI: 104512; Tnfrsf4.

DR InterPro: IPR001368; TNFR_c6.

DR Pfam: PF00020; TNFR_c6; 3.

DR ProDom: PD000771; TNFR_c6; 1.

DR SMART: SM00208; TNFR_3.

DR PROSITE: PS00652; TNFR_NGFR_1; 3.

DR PROSITE: PS50050; TNFR_NGFR_2; 2.

DR KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;

KW Signal.

FT SIGNAL 1 19

FT CHAIN 20 272

FT DOMAIN 20 272

FT TRANSMEM 212 236

FT DOMAIN 237 272

FT DOMAIN 26 165

FT REPEAT 26 61

FT REPEAT 62 103

FT REPEAT 104 124

FT REPEAT 125 165

FT CARBOHYD 144 144

FT CONFLICT 15 15

FT SEQUENCE 272 AA; 30153 MW; 06E7BA4156F0D08E CRC64;

Query Match 13.7%; Score 215.5; DB 1; Length 272;

Best Local Similarity 31.5%; Pred. No. 1.5e-10;

Matches 46; Conservative 17; Mismatches 58; Indels 25; Gaps 5;

OY 41 SCKEDRYPVGSECCPCPCSPGYRYKACGELGTVCPCPPGYIAHLNGISKLCQCMCD 100

DB 26 NCVKHTYPSCHKRCQCPGSHVSRCDHTRDYLCHPCETGFYNEAVN-YDCKQCTQCN 84

OY 101 PANGLASRNCSTENAVGCGSPGHFCIYQDDGHCACATAYATSSGQRYQKGTESQDT 160

DB 85 HRSGLKONCTPTDTCVCRPG-----TOP--RQDSGYKLGVN- 122

OY 161 LCONCPGTFSPNGTLECOHOTKCS 186

DB 123 -CVPCPGHFSF-GNNACKPMTNCT 146

RESULT 14

TNR2_MOUSE

AC P25119; P97893; STANDARD; PRT; 474 AA.

DT 01-MAY-1992 (Rel. 22, Created)

DT 01-MAY-1992 (Rel. 22, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TNF-R2) (P75).

GN TNFRSF1B OR TNFR2 OR TNFR-2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_Taxid=10090;

RN [1]

RX SEQUENCE FROM N.A.

RA MEDLINE-91187885; PubMed-1849278;

RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C., Wong G.H., Chen E.Y., Goeddel D.V.;

RT "Cloning and expression of cDNAs for two distinct murine tumor necrosis factor receptors demonstrate one receptor is species specific."

RT Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).

RL [2]

RN SEQUENCE FROM N.A.

RX MEDLINE-91246168; PubMed-1645445;

RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I., Copeland N.G., Jenkins N.A., Smith C.A.;

RT "Molecular cloning and expression of the type 1 and type 2 murine receptors for tumor necrosis factor."

RT Mol. Cell. Biol. 11:3020-3026(1991).

RL [3]

RN SEQUENCE OF 1-26 FROM N.A.

RC STRAIN=MOD;

RA Jacob C.O., Liu J.;

RL Submitted (JAN-1996) to the EMBL/Genbank/DBJ databases.

RN [4]

RX SEQUENCE OF 1-22 FROM N.A.

RC TISSUE=Liver;

RA Kissenevghis M., Fellows R., Feldmann M., Chernajovsky Y.;

RL Submitted (MAY-1995) to the EMBL/Genbank/DBJ databases.

CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA.

CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

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CC

DR EMBL: M60459; AAA39752.1; -

DR EMBL: M59378; AAA40463.1; -

DR EMBL: U39488; AAA85021.1; -

DR EMBL: X87128; CAA60618.1; -

DR PIR: B38634; B38634.

DR HSSP: P19438; INCF.

DR MGI: 131483; Tnfrsf1b.

DR InterPro: IPR001368; TNFR_c6.

DR Pfam: PF00071; TNFR_c6; 4.

DR ProDom: PD000771; TNFR_c6; 1.

DR SMART: SM00208; TNFR_4.

DR PROSITE: PS00652; TNFR_NGFR_1; 2.

DR PROSITE: PS50050; TNFR_NGFR_2; 3.

DR KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.

KW SIGNAL 1 22

FT CHAIN 23 474

FT DOMAIN 23 258

FT TRANSMEM 259 288

FT DOMAIN 289 474

FT DOMAIN 39 203

FT REPEAT 39 77

FT REPEAT 78 119

FT REPEAT 120 164

FT REPEAT 165 203

FT DISULFID 40 54

FT DISULFID 55 68

FT DISULFID 58 76

FT DISULFID 79 94

TUMOR NECROSIS FACTOR RECEPTOR 2.

EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

4 X TNFR-CYS.

TNFR-CYS 1.

TNFR-CYS 2.

TNFR-CYS 3.

TNFR-CYS 4.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

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CC DISULFID 97 111 BY SIMILARITY.
CC DISULFID 101 119 BY SIMILARITY.
CC DISULFID 121 127 BY SIMILARITY.
CC DISULFID 136 145 BY SIMILARITY.
CC DISULFID 139 163 BY SIMILARITY.
CC DISULFID 166 181 BY SIMILARITY.
CC CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 474 AA: 50319 MW: 462EA8398C4D6563 CRC64;

Query Match 13.5%; Score 213.5; DB 1; Length 474;
Best Local Similarity 28.5%; Pred. No. 3.5e-10;
Matches 55; Conservative 20; Mismatches 101; Indels 17; Gaps 6;

QY 20 VLRLVLYLFLCAPCYAPALPSCKEDEY--PYGSE-----CCPKSPGYRKEAGE 69
DB 11 VELDLMLMGTHTPAQVVLTPKPEPGYECQISOEYDRKACQCAKCPGQYVHFCKK 70
QY 70 LRGVCEPCPGTGYIAHLNGLSKLOC--QMGDPAMGLASRNCSTENAVGCSPGHRC 127
DB 71 TSDTVACDCEASMTYQVWNOFTCLSCSSCTTDOVEIRA--CTKQQRVCACAGRYC 127
QY 128 IVQ-DGDHCAACRAYATSSPGQVOKGTEGSDTLQONCPGTFSPNGTLECOHOTFC 185
DB 128 AKHTSGSGROCMRLSKCGPFGVASSRAPNGNVLCACAPGTFSDTTSITVCRPHRC 187
QY 186 SWLVTKAGAGTSS 198
DB 188 SILAIPGNASTDA 200

RESULT 15
FSA_RAT STANDARD: PRT: 324 AA.
AC 063199;
AC 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
DE (APO-1 ANTIGEN) (CD95).
GN TNFRSF6 OR PT1 OR FAS.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SPRAGUE-DAWLEY; TISSUE=Liver;
RX MEDLINE=94128114; PubMed=7507668;
RA Kimura K., Yamamoto M., Wakatsuki T.;
RT "A variant mRNA species encoding a truncated form of Fas antigen in
RT the rat liver.";
RL Biochem. Biophys. Res. Commun. 198;666-674(1994).
CC -!- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE
CC ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED
CC RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING
CC SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC
CC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF
CC CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING
CC APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
CC INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
CC SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -!- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC -!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D26112; BAA05108.1; -.
CC InterPro: IPR000488; Death.
CC InterPro: IPR001368; TNFR_c6.
CC Pfam: PF00531; death; 1.
CC DR Pfam; PF00020; TNFR_c6; 3.
CC SMART; SM00005; DEATH; 1.
CC SMART; SM00208; TNFR; 3.
CC DR PROSITE; PS00652; TNFR_NGFR_1; 2.
CC DR PROSITE; PS00505; TNFR_NGFR_2; 2.
CC DR PROSITE; PS50017; DEATH_DOMAIN; 1.
CC KW Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal.
CC FT SIGNAL 1 21 BY SIMILARITY.
CC FT CHAIN 22 324 FAST RECEPTOR.
CC FT DOMAIN 22 171 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 172 188 POTENTIAL.
CC FT DOMAIN 189 324 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 43 163 3 X TNFR-CYS.
CC FT REPEAT 43 79 TNFR-CYS 1.
CC FT REPEAT 80 123 TNFR-CYS 2.
CC FT REPEAT 124 163 TNFR-CYS 3.
CC FT DOMAIN 219 303 DEATH.
CC FT CARBOHYD 43 43 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 114 114 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 324 AA: 36835 MW: D25D583C909D09 CRC64;

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Query Match 13.1%; Score 206.5; DB 1; Length 324;
Best Local Similarity 24.7%; Pred. No. 9.1e-10;
Matches 58; Conservative 27; Mismatches 93; Indels 57; Gaps 6;

QY 41 SCKEDYVPGSECPKSPGYRKEACGLTGT-VCEPCPPG-TYIAHLNGLSKLOCQ 98
DB 43 NCSEELVQVPPCCPCQPGERKVKDCITSSGAPLPCHEETDTRKHNSDKCRRCF 102
QY 99 CDPAMGLASRNCSTENAVGCCSPGHCTIVDGDHCAACRAYATSSPGQVOKGTEG 158
DB 103 CDEGHGLEVEETNCTPTONTKCRCKENFYCNASLGDHCYHC---TSCGLDILPECTRTS 158
QY 159 DTLQONCPGTFSPNGTLEEOHQKCSWLTVKACAGTSSSHWMMPLSGSLVIYICST 218
DB 159 NTKCKK-----OSSNKLMLL-----ILPGL 180
QY 219 VGLICVRRKRGDVVKIVVSQRRQEAEGEATVIALQAPDVTVAVEETI 273
DB 181 ALTFVFIYKR-----YKRRQPGDESGITPESVPMNVSDVNLNKYI 222

```

Search completed: January 24, 2002, 16:25:16
 Job time: 191 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 24, 2002, 16:21:45 ; Search time 23.81 Seconds
(without alignments)
1738.558 Million cell updates/sec

Title: US-08-741-095B-26

Perfect score: 1578
Sequence: 1 MEPPGDMGPPMRSTPRTDV.....VTTVAVEETIPSTGSPNH 283

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP.TREMBL_17:*
2: sp.archaea:*
3: sp.bacteria:*
4: sp.fungi:*
5: sp.human:*
6: sp.invertebrate:*
7: sp.mammal:*
8: sp.mhc:*
9: sp.organelle:*
10: sp.phage:*
11: sp.plant:*
12: sp.podent:*
13: sp.virus:*
14: sp.vertebrate:*
14: sp.unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
1	1303.5	82.6	283	6 Q9XSZ8	Q9XSZ8 cercopithec
2	271.5	17.2	349	12 057100	057100 monkeypox v
3	269.5	17.1	348	12 057277	057277 monkeypox v
4	269.5	17.1	348	12 057108	057108 monkeypox v
5	269.5	17.1	349	12 057291	057291 monkeypox v
6	269.5	17.1	349	12 057101	057101 monkeypox v
7	269.5	17.1	349	12 057102	057102 monkeypox v
8	268.5	17.0	222	11 099NE1	099NE1 mus musculu
9	268.5	17.0	234	11 099NE2	099NE2 mus musculu
10	266.5	16.9	349	12 057284	057284 camelipox vi
11	266.5	16.9	349	12 057098	057098 camelipox vi
12	265.5	16.8	348	12 057103	057103 monkeypox v
13	265.5	16.8	349	12 057099	057099 monkeypox v
14	265	16.8	260	11 099NE0	099NE0 mus musculu
15	262.5	16.6	349	12 057097	057097 camelipox vi
16	262	16.6	169	11 099KE0	099KE0 ratius norv
17	259	16.4	349	12 057111	057111 variola vir
18	257.5	16.3	348	12 057112	057112 variola vir
19	257.5	16.3	348	12 085407	085407 variola vir

20	257.5	16.3	351	12 057117	057117 compox viru
21	257	16.3	349	12 057110	057110 variola vir
22	257	16.3	349	12 089118	089118 variola vir
23	257	16.3	349	12 089098	089098 variola vir
24	254.5	16.1	425	4 Q16042	Q16042 homo sapien
25	254.5	16.1	438	13 Q9DFV0	Q9DFV0 brachydantio
26	251.5	15.9	203	11 099NE3	099NE3 mus musculu
27	249.5	15.8	203	4 09BYU0	09BYU0 homo sapien
28	249	15.8	349	12 057109	057109 variola vir
29	246	15.6	300	4 095407	095407 homo sapien
30	243.5	15.4	351	12 073559	073559 compox viru
31	239	15.1	350	12 057116	057116 compox viru
32	236.5	15.0	351	12 057121	057121 compox viru
33	232.5	14.7	349	12 057305	057305 compox viru
34	228.5	14.5	326	12 057122	057122 compox viru
35	229	14.5	347	12 057119	057119 compox viru
36	228.5	14.5	326	12 057120	057120 compox viru
37	228	14.4	312	13 09DGH8	09DGH8 gallus gall
38	228	14.4	360	12 057118	057118 compox viru
39	227	14.4	285	13 09DGH7	09DGH7 gallus gall
40	226.5	14.4	350	12 057123	057123 compox viru
41	225.5	14.3	347	12 057115	057115 compox viru
42	225.5	14.3	355	12 085308	085308 compox viru
43	219.5	13.9	267	6 002764	002764 oryctolagus
44	219.5	13.9	319	6 09TV79	09TV79 oryctolagus
45	218	13.8	320	6 09XS29	09XS29 oryctolagus

ALIGNMENTS

RESULT 1
ID Q9XSZ8 PRELIMINARY; PRT: 283 AA.
AC Q9XSZ8;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE HVENS.
GN HVENS.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheciinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RX MEDLINE=99296730; PubMed=10366573;
RA Foster T.P., Chouljenko V.N., Kousoulas K.G.;
RT "Functional characterization of the Hvea homolog specified by African
RT green monkey kidney cells with a herpes simplex virus expressing the
RT green fluorescence protein.";
RL Virology 258:365-374(1999).
DR EMBL: AF147720; AAD37381.1;
DR HSSP: P25942; ICDP.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 3.
DR ProDom: PD000771; TNFR_c6; 1.
DR SMART: SMO0208; TNFR_3.
DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
SO SEQUENCE 283 AA; 30199 MW; 397951C6617EE3AA CRC64;

Query Match 82.6%; Score 1303.5; DB 6; Length 283;
Best Local Similarity 82.0%; Pred. No. 4.4e-116;
Matches 232; Conservative 18; Mismatches 30; Indels 3; Gaps 2;

OY 1 MEPPGDMGPPMRSTPRTDVLRVLVTLFLGAPCYAPALPSCKEDEYVSGSECCPKCSPG 60
||||| ||| | : : | ||||| : ||||| ||||| ||||| ||
Db 1 MEPPGDMGPPMRSTPRTDVLRVLVTLFLGSSCYAPALPSCKEDEYVSGSECCPKCSPG 60

```

QY 61 YRVKACGELTGTVCPCPGTYIAHLNGLSKLOCOMCDPAMGLASRNCSTENAVCG 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 FHVROACGOTGTVCPCPGTYIAHLNGLSKLOCOMCDPAMGLTRSRNCSTTANALCG 120
QY 121 CSPGHFCITVODGDHCAACRAVATSPGQRYOKGTEGSDTLQNCPPGTFSPNGLEECQ 180
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 CSPGHFCITVODGDHCAACRAVATSPGQRYOKGTEGSDTLQNCPPGTFSSNGLEECQ 180
QY 181 HOTKCS-MVTAGAGCTSSSHWMMFLSGSLVIVYCSIV--GLIICVARRKRGDVAVY 237
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 181 HGKCKMVLTEGPGTSSRWMMFLSGSLVIVYGLIILILICVARRKSRGDVAVY 240
QY 238 IYSVORRQEAEGEATVIALQAPDVTVAVEETIPSTGSR 280
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 241 IYSVORRQEAEGEATVIALQAPDVTVAVEETIPSTGSR 283

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RESULT 2
057100 PRELIMINARY; PRT; 349 AA.
AC 057100;
DT 01-JUN-1998 (TREMblrel. 06, Created)
DE 01-JUN-1998 (TREMblrel. 17, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NIGERIA-1971 (71-0082);
RL Loparev V.N., Parsons J.M., Esposito J.J.;
   Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL; U87842; AAB94361.1; -.
DR HSSP; P25942; ICDF.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR_2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 349 AA; 38239 MW; DFC280D478F2422 CRC64;

```

```

Query Match 17.2%; Score 271.5; DB 12; Length 349;
Best Local Similarity 32.6%; Pred. No. 7.6e-18;
Matches 59; Conservative 23; Mismatches 80; Indels 19; Gaps 5;

QY 21 LRLVLYLFLGAPC-----YAPALPSCKEDEYPVGSECCPKSPGYRVKACGEL 70
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MSVLYSYLLFLSCITINGRDLAPHAPNSGKCKDNEYRSRNLCCISCSPGTAYASRLCDSK 60
QY 71 TGTVCPCPGTYIAHLNGLSKLOQ--MCDPAMGLASRNCSTENAVCGSPGHFCIT 129
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 TTNQCTPCGSDFTSHNNHLQACLSCNGRCD--SNQVETRSCNTTHNRICECSPGYCYLL 118
QY 130 QGDGHCACRAVATSPGQRYOKGTEGSDTLQNCPPGTFSPNGLEECQHOTKCSMLV 189
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 119 KGASGCTICISHTKCGIGYV--SGYTSIDGVLCSPCGPGTYS-----HTVSSTDKCEPV 172
QY 190 T 190
Db 173 T 173

```

```

RESULT 3
057277 PRELIMINARY; PRT; 348 AA.
AC 057277;
DT 01-JUN-1998 (TREMblrel. 06, Created)
DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)

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DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ZAIRE-1996(96-17), Zaire-1996 (96-16);
RL Loparev V.N., Parsons J.M., Esposito J.J.;
   Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL; U87841; AAB94358.1; -.
DR HSSP; P25942; ICDF.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR_2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 348 AA; 38212 MW; 54019521556C2D8F CRC64;

```

```

Query Match 17.1%; Score 269.5; DB 12; Length 348;
Best Local Similarity 32.6%; Pred. No. 1.2e-17;
Matches 57; Conservative 25; Mismatches 78; Indels 15; Gaps 5;

QY 21 LRLVLYLFLGAPC-----YAPALPSCKEDEYPVGSECCPKSPGYRVKACGEL 70
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MSVLYSYLLFLSCITINGRDLAPHAPNSGKCKDNEYRSRNLCCISCSPGTAYASRLCDSK 60
QY 71 TGTVCPCPGTYIAHLNGLSKLOQ--MCDPAMGLASRNCSTENAVCGSPGHFCIT 129
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 TTNQCTPCGSDFTSHNNHLQACLSCNGRCD--SNQVETRSCNTTHNRICECSPGYCYLL 118
QY 130 QGDGHCACRAVATSPGQRYOKGTEGSDTLQNCPPGTFSPN-GTLEECQHOT 183
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 119 KGSSGCTICISHTKCGIGYV--SGYTSIDGVLCSPCGPGTYSHTVSSYTDKCEPV 172

```

```

RESULT 4
057108 PRELIMINARY; PRT; 348 AA.
AC 057108;
DT 01-JUN-1998 (TREMblrel. 06, Created)
DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
DE 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ZAIRE-1970 (CONGO-8);
RL Loparev V.N., Parsons J.M., Esposito J.J.;
   Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL; U88142; AAB94367.1; -.
DR HSSP; P25942; ICDF.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR_2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 348 AA; 38212 MW; E555979057DEC91F CRC64;

```

```

Query Match 17.1%; Score 269.5; DB 12; Length 348;
Best Local Similarity 32.6%; Pred. No. 1.2e-17;
Matches 57; Conservative 25; Mismatches 78; Indels 15; Gaps 5;

```

```

Oy 21 LRLVLYLFLFELGAPC-----VAPALPSCKEDPEYPAVGSCCPKSPGRVKNEACGEL 70
    :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MRSVLXSTLLFLSCILLINGRDIAPHPAPSNGKKDNEYRNKLCCCLSCPPTGYATSLRCDSK 60
    :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 71 TGVCEPCPPGTIYAHLNGLSKLCLOQ-MCDPAMGLRASRNCSTRENAVCGSPGHCTIV 129
    :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 TNYOCTPGSGDFETSHNNHLOACLSCNGRCD--SNQVERSCNTTHNRILCECSPPGYCILL 118
    :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Oy 130 ODGDHCACRAATATSSPGORVKGSTESODTLCQNCPPTESPNN-CTLPECOHOT 183
    :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 119 KGSSECRCICISXTKCGIGCY-SGITSTGDVICSPGPETYSHTVYSTDKCEPYT 172
    :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT      5
ID 057291          PRELIMINARY;           PRT;       349 AA.
AC 057291;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_Taxid=10244;
   [1]
RM SEQUENCE FROM N.A.
RP STRAIN-VARIOUS STRAINS;
RC Loparev V.N., Parsons J.M., Esposito J.J.;
RL Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: U88144: AAB94369.1; -
DR EMBL: U87842: AAB94359.1; -
DR EMBL: U87894: AAB94365.1; -
DR EMBL: U87995: AAB94366.1; -
DR EMBL: U88143: AAB94368.1; -
DR HSSP: P25942: ICDF.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 2.
DR ProDom: PD000771; TNFR_c6; 1.
DR SMART: SM00208; TNFR_2.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE      349 AA; 38295 MW; CBD2C949EDB8E7C CRC64;
```

Query Match	17.1%	Score 269.5	DB 12	Length 349	
Best Local Similarity	32.6%	Pred. No. 1.2e-17			
Matches 59	Conservative	22	Mismatches 81	Indels 19	Gaps 5
QY	21	LRLVLYLFLGAPC-----YAPALPSCREDEYPVGSCEPCSPGYRVEKCEGEL	70		
Db	1	MSRVSYSLFLSCIIINGRDIAPIHAPSPNGKCKDNEYRSRNLCCLSCPGTVASRLCDSEK	60		
QY	71	TGTGCEPPPTGYIAHLNGLSKLCCQ--MCDPAMBLRASRNCSSRLENATVCGSGPHGFCIV	129		
Db	61	TNTQCTPGCSPTFVSHNNHLQACLSGNGRCD--SNQVETRSCNTHHNRKICECSPGYICLL	118		
QY	130	QDGDHCACRAVYATSSPGQRYQKGGTESODTLQONCPPTGEPSPNGLTLEECQHQTKCSMWL	189		
Db	119	KGASGCRFCISIKTKGIGYGV--SGYTSIGDVLCSPCGPETS-----HIVSSTDKCEPVV	172		
QY	190	T 190			
Db	173	T 173			
RESULT	6				
ID	057101	PRELIMINARY	PRT	349	AA
AC	057101				
DT	01-JUN-1998	(TREMBlrel. 06, Created)			

DT 01-JUN-1998 (TREMBLrel. 06, last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
 GN Crmb.
 OS Monkeypox virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 CC Orthopoxvirus.
 OX NCBI_TaxID=10244;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ZAIRE-1977 (77-0666);
 RA Loparev V.N., Parsons J.M., Esposito J.J.;
 RL Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.
 DR EMBL: U87845; AAB94362.1; -
 DR HSSP: P25942; ICDF.
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF00020; TNFR_c6; 2.
 DR ProDom: PD000771; TNFR_c6; 1.
 DR SMART: SMO0208; TNFR; 2.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS0050; TNFR_NGFR_2; 2.
 SQ SEQUENCE. 349 AA; 38311 MW; 0265B00CFB858BE CRC64;

```

Query Match      17.1% Score 269.5; DB 12; Length 349;
Best Local Similarity 32.6%; Pred. No. 1,2e-17;
Matches 59; Conservative 22; Mismatches 81; Indels 19; Gaps 5

OY 21 LRLVLYLFFLAGPC-----YAPALPSCKEDEYPVGSECCPKCSBGYRVKREAGEL 70
    | :| | | | :| | :| | :| | | |
DB 1 MSRSVSYLYLFSLCTIINGRDIAPIHAPSNGCKDNERYSRNLCLTCLSCPITYAARICDJSK 60
    | :| | | | | :| | | | | :| | | | |
OY 71 TGTVEPECPGGTYIAHLNLSKLCLOQ-MCDPAMGLRAARNCSRPNNAVCSSPGHFCLV 129
    | :| | | | | | :| | | | | :| | | | |
DB 61 TMTQCTPCGSDFTTHNNHLAQACLSGNCRGD--SNQVETRSCNTTHNRRCESPSGYCILL 118
    | :| | | | | | | :| | | | | :| | | | |
OY 130 QDGDIACACRAATSSPGCARVKGSGTESODTLCONCPPTFSPNGNLIECOHQOTKSMWLV 189
    | :| | | | | | | :| | | | | :| | | | |
DB 119 KSSSGCRMCISAKTKGIGIV-SGTSTSDVICSPCGPETYS----HTVSSTDKCEPVV 172
    | :| | | | | | | :| | | | | :| | | | |
OY 190 T 190
DB 173 T 173

```

```

RESULT 7
ID 057102 PRELIMINARY: PRT: 349 AA.
AC 057102;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
CX NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BEIN-1978 (78-3945);
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RL Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL: U87846; AAB94363.1; -.
DR HSSB: F25942; ICDF.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 2.
DR ProDom: PD000771; TNFR_c6; 1.
DR SMART: SM00208; TNFR: 2.
DR ProSite: PS00652; TNFR_NGFR_1; 2.
DR ProSite: PS50050; TNFR_NGFR_2; 2.
SO SEQUENCE 349 AA; 38308 MW; CBD2C94F994C59C CRC64;

```



```

OY 21 LRLVLYLFLGAPC-----YAPALPSCKEDEYPVGSCECPKCSBPGYRVKEACGEL 70
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 1 MRSVLYSTYLFSLCIIINGRDVTPYAPSNKGCKDNEYSRNKLCCISCPGTYASRLCDSK 60
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 71 TGTVEPCPPGTYIAHLNGLSKLCLOQ-MCDPAMGLRASRNCSTRENNAVCGSPGHFCTIV 129
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 61 TMTGCTPGSGDFTSHNNHLQACLSGNGRCD--SNQVETRSCNTTHNRICECSPGYCYLL 118
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 130 QGDHCAACRAVATSSPGORVOKGTESEDITLCQNCPEGTSPN-GTLEECQ 180
   :|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 119 KSSSGCKACVSGTKGIGYV-SGHTSADYICSPGIGTYSRTVSSADKCE 169
   :|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

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RESULT 11

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057098 PRELIMINARY: PRT: 349 AA.
AC 057098:
DT 01-JUN-1998 (TREMblrel. 06, Created)
DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN CRM.
OS Camelpox virus (strain CP-1).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_Taxid=28873;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SAUDI-M3;
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RL Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL: U87839; AAB94356.1; -.
DR HSSP: P25942; ICDF.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 2.
DR ProDom: PD000771; TNFR_c6; 1.
DR SMART: SM00208; TNFR_2.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 349 AA: 37978 MW: 8630FEAD7A584B5 CRC64;

```

```

Query Match 16.9%; Score 266.5; DB 12; Length 349;
Best Local Similarity 33.1%; Pred. No. 2.3e-17;
Matches 57; Conservative 24; Mismatches 76; Indels 15; Gaps 5;

```

```

OY 21 LRLVLYLFLGAPC-----YAPALPSCKEDEYPVGSCECPKCSBPGYRVKEACGEL 70
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 1 MRSVLYSTYLFSLCIIINGRDVTPYAPSNKGCKDNEYSRNKLCCISCPGTYASRLCDSK 60
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 71 TGTVEPCPPGTYIAHLNGLSKLCLOQ-MCDPAMGLRASRNCSTRENNAVCGSPGHFCTIV 129
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 61 TMTGCTPGSGDFTSHNNHLQACLSGNGRCD--SNQVETRSCNTTHNRICECSPGYCYLL 118
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 130 QGDHCAACRAVATSSPGORVOKGTESEDITLCQNCPEGTSPN-GTLEECQ 180
   :|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 119 KSSSGCKACVSGTKGIGYV-SGHTSADYICSPGIGTYSRTVSSADKCE 169
   :|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

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RESULT 12

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057103 PRELIMINARY: PRT: 348 AA.
AC 057103:
DT 01-JUN-1998 (TREMblrel. 06, Created)
DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN CRM.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_Taxid=10244;
RN [1]

```

```

RP SEQUENCE FROM N.A.
RC STRAIN=ZAIRE-1979 (79-0005);
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RL Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL: U87847; AAB94364.1; -.
DR HSSP: P25942; ICDF.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 2.
DR ProDom: PD000771; TNFR_c6; 1.
DR SMART: SM00208; TNFR_2.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 348 AA: 38184 MW: 34A5E68B27907B5 CRC64;

```

```

Query Match 16.8%; Score 265.5; DB 12; Length 348;
Best Local Similarity 32.0%; Pred. No. 2.8e-17;
Matches 56; Conservative 25; Mismatches 79; Indels 15; Gaps 5;

```

```

OY 21 LRLVLYLFLGAPC-----YAPALPSCKEDEYPVGSCECPKCSBPGYRVKEACGEL 70
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 1 MRSVLYSTYLFSLCIIINGRDVTPYAPSNKGCKDNEYSRNKLCCISCPGTYASRLCDSK 60
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 71 TGTVEPCPPGTYIAHLNGLSKLCLOQ-MCDPAMGLRASRNCSTRENNAVCGSPGHFCTIV 129
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 61 TMTGCTPGSGDFTSHNNHLQACLSGNGRCD--SNQVETRSCNTTHNRICECSPGYCYLL 118
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 130 QGDHCAACRAVATSSPGORVOKGTESEDITLCQNCPEGTSPN-GTLEECQHOT 183
   :|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 119 KSSSGCKRCISMTKCGIGYV-SGYTSGDYICSPCGTYSHTVSSDCKEPTV 172
   :|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

```

RESULT 13

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057099 PRELIMINARY: PRT: 349 AA.
AC 057099:
DT 01-JUN-1998 (TREMblrel. 06, Created)
DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN CRM.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_Taxid=10244;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SIERRA LEONE-1970 (70-0266);
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RL Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL: U87843; AAB94360.1; -.
DR HSSP: P25942; ICDF.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 2.
DR ProDom: PD000771; TNFR_c6; 1.
DR SMART: SM00208; TNFR_2.
DR PROSITE: PS00652; TNFR_NGFR_1; 2.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 349 AA: 38321 MW: FE49028CC933F57 CRC64;

```

```

Query Match 16.8%; Score 265.5; DB 12; Length 349;
Best Local Similarity 32.6%; Pred. No. 2.8e-17;
Matches 59; Conservative 22; Mismatches 81; Indels 19; Gaps 5;

```

```

OY 21 LRLVLYLFLGAPC-----YAPALPSCKEDEYPVGSCECPKCSBPGYRVKEACGEL 70
   ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 1 MRSVLYSTYLFSLCIIINGRDVTPYAPSNKGCKDNEYSRNKLCCISCPGTYASRLCDSK 60
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 71 TGTVEPCPPGTYIAHLNGLSKLCLOQ-MCDPAMGLRASRNCSTRENNAVCGSPGHFCTIV 129
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 61 TMTGCTPGSGDFTSHNNHLQACLSGNGRCD--SNQVETRSCNTTHNRICECSPGYCYLL 118
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

```

QY 130 QDGDHCAACRAVATSSPGQGVOKGTESDTLQNCPPGTFSPNGTLEBCHQHTKCSMLV 189
 DB 119 KGALGCRCTISKTKGIGYGV-SGYTSTGDVICSPPCGPTYS-----HTVSTDKCEPV 172
 QY 190 T 190
 DB 173 T 173

RESULT 14

Q99NEO PRELIMINARY: PRT: 260 AA.
 ID Q99NEO;
 AC Q99NEO;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)
 DE CD40 TYPE V ISOFORM.
 GN CD40.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=211172023; PubMed=11172023;
 RA Tone M., Tone Y., Fairchild P.J., Wykes M., Waldmann H.;
 RT "Regulation of CD40 function by its isoforms generated through
 RT alternative splicing."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001).
 DR EMBL; AJ401390; CAC29430.1; -
 SQ SEQUENCE 260 AA; 28895 MW; 57A5BACE8CF2F546 CRC64;

Query Match 16.8%; Score 265; DB 11; Length 260;
 Best Local Similarity 28.5%; Pred. No. 2.3e-17;
 Matches 68; Conservative 34; Mismatches 95; Indels 42; Gaps 8;

QY 41 SCKEDEVPGSECCPKSPGYRVKACGELTGVCPCPPGTIYIAHLNGLSKLOCOMCD 100
 DB 25 TCSDKQYLYHDGQCCDLCQPSRLTSHCTALEKIQCHPCDSGERSAOMNRIRCHQHRCE 84
 QY 101 PANGLRASRNCSTENAVAGCSPGHFCIVODGDHCAACRAVATSSPGQGVOKGTESDTL 160
 DB 85 PNGGLRVKKEGTAEEDVTCCKEGQCHTCKSD--CEACAQHTPCICPGVEMATEETTD 141
 QY 161 LQNCPPGTFSPNGTLEBCHQHTKCS-----WLVTKAGACTSSHWVWFLSGSLVIYV 215
 DB 142 VCHPCVPGFSSNQSLEKCYPTWTCEDKNLEVLQK--GTSQTN----- 183
 QY 216 CSTVGLIICVK-RRKPRGDVVKVIVSVORRQBAEGEATVIALQAPPDVTVAVEETI 273
 DB 184 -----VICKEVYKKPKDN--EMLPPARRODPQEME-----DYFGHTAAPVOETL 227

RESULT 15

Q57097 PRELIMINARY: PRT: 349 AA.
 ID Q57097;
 AC Q57097;
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, last sequence update)
 DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
 GN CRM6.
 OS Camelpox virus (strain CP-1).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=28873;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IRAN (CP-1);
 RA Loparev V.N., Parsons J.M., Esposito J.J.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U87838; AAB94355.1; -

DR HSSP; P25942; 1CDF.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 2
 DR PRODOM; PD000771; TNFR_c6; 1.
 DR SMART; SM00208; TNFR; 3.
 DR PROSITE; PS00652; TNFR_NGFR_1; 1.
 DR PROSITE; PS00650; TNFR_NGFR_2; 2.
 SQ SEQUENCE 349 AA; 37944 MW; 829EA54EDAC60455 CRC64;

Query Match 16.6%; Score 262.5; DB 12; Length 349;
 Best Local Similarity 33.1%; Pred. No. 5.4e-17;
 Matches 57; Conservative 23; Mismatches 77; Indels 15; Gaps 5;

QY 21 LRVLVLTFLGARC-----YAPALPSCKEDEVPGSECCPKSPGYRVKACGEL 70
 DB 1 MKSVLSYILFLSCIIINGEDVTPYAPSNQCKDNEYKRRHNLCLSCPPGTASRLCDSK 60
 QY 71 TGVCPCPPGTIYIAHLNGLSKLOCO-MCDPAMGLRASRNCSTENAVAGCSPGHFCIV 129
 DB 61 TNYQCTPCGSGTITSNNHLPACLSGNGRCD--SNQVETRSCWTTNRRICEGSPGYICIL 118
 QY 130 QDGDHCAACRAVATSSPGQGVOKGTESDTLQNCPPGTFSPN-GTLEECQ 180
 DB 119 KGSSGCKACVSKTKGIGYGV-SGHTSAGDVICSPPGLGTSRTVSADKCE 169

Search completed: January 24, 2002, 16:25:00
 Job time: 195 sec

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